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QM nucleic - nucleic search, using sw model

Run on: February 22, 2005, 19:20:42 ; Search time 110 Seconds
(without alignments)
8895.395 Million cell updates/sec

Title: US-09-920-953-2
Perfect score: 598
Sequence: 1 ggcctcgcagacgcgc.....agccatttcgacccaagcc 598

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1202784 seqs, 818138359 residues
Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA:
1: /cgn2_6/ptodata/1/ina/5A COMB.seq.*
2: /cgn2_6/ptodata/1/ina/5B COMB.seq.*
3: /cgn2_6/ptodata/1/ina/6A COMB.seq.*
4: /cgn2_6/ptodata/1/ina/6B COMB.seq.*
5: /cgn2_6/ptodata/1/ina/PTCUS COMB.seq.*
6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	97.2	16.3	381	4	US-09-902-540-5776
2	97.2	16.3	72704	4	US-09-902-540-1273
3	46.4	7.8	4403765	3	US-09-103-840A-2
4	46.4	7.8	4411529	3	US-09-103-840A-1
5	45.2	7.6	1143	4	US-09-902-540-8600
6	45.2	7.6	6821	4	US-09-902-540-907
7	43.4	7.3	603	4	US-09-902-540-14
8	43.4	7.3	603	4	US-09-902-540-5853
9	42.8	7.2	585	4	US-09-902-540-3555
10	42.8	7.2	19019	4	US-09-902-540-1171
11	42.6	7.1	3128	4	US-08-744-072-1
12	42.4	7.1	26896	4	US-09-949-016-16800
13	42.2	7.1	759	4	US-09-252-991A-11092
14	42	7.0	1058	3	US-09-452-239-11
15	41.6	7.0	969	4	US-09-902-540-8164
16	41.6	7.0	1280	3	US-09-096-776B-4
17	41.6	7.0	1280	4	US-09-923-922-4
18	41.6	7.0	1491	3	US-09-082-092-9
19	41.6	7.0	1491	4	US-09-885-722A-9
20	41.6	7.0	1524	3	US-08-840-767-3
21	41.6	7.0	1817	3	US-09-288-292A-45
22	41.6	7.0	2887	4	US-09-679-298A-1
23	41.6	7.0	3083	2	US-08-480-994-36
24	41.6	7.0	3083	2	US-08-616-844-36
25	41.6	7.0	3083	2	US-08-599-654-36
26	41.6	7.0	3083	2	US-08-485-573-36
27	41.6	7.0	3083	3	US-08-944-868A-36

28	41.6	7.0	3083	3	US-08-944-423A-36	Sequence 36, Appl
29	41.6	7.0	3083	3	US-08-925-743-36	Sequence 36, Appl
30	41.6	7.0	3083	3	US-08-944-496-36	Sequence 36, Appl
31	41.6	7.0	3083	3	US-08-925-767-36	Sequence 36, Appl
32	41.6	7.0	3084	3	US-08-826-246-11	Sequence 11, Appl
33	41.6	7.0	3084	3	US-08-944-495-11	Sequence 11, Appl
34	41.6	7.0	3084	3	US-09-126-640-6	Sequence 6, Appl
35	41.6	7.0	3084	3	US-08-925-588-11	Sequence 11, Appl
36	41.6	7.0	3084	3	US-09-288-292A-6	Sequence 6, Appl
37	41.6	7.0	3084	4	US-09-372-044-11	Sequence 11, Appl
38	41.6	7.0	3084	4	US-08-825-486-11	Sequence 11, Appl
39	41.6	7.0	3084	4	US-08-826-248-11	Sequence 839, App
40	41.6	7.0	5663	4	US-09-902-540-839	Sequence 9635, Ap
41	41.2	6.9	3066	4	US-09-902-540-9635	Sequence 1094, Ap
42	41.2	6.9	15782	4	US-09-902-540-9640	Sequence 9640, Ap
43	41	6.9	1440	4	US-09-902-540-1094	Sequence 1094, Ap
44	41	6.9	15782	4	US-09-902-540-1094	Sequence 1094, Ap
45	40.8	6.8	792	4	US-09-252-991A-10543	Sequence 10543, A

ALIGNMENTS

RESULT 1
US-09-902-540-5776
; Sequence 5776, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5776
; LENGTH: 381
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
US-09-902-540-5776

Query Match	16.3%;	Score	97.2;	DB	4;	Length	381;
Best Local Similarity	56.9%;	Pred. No.	2.7e-17;				
Matches	199;	Conservative	0;	Mismatches	148;	Indels	3;
Gaps	1;						
QY	61	AAGAAGCTGTTT	GATGACCTTGGCGGCGGAGGAGGATGAAGCTGGCGGTGACACCTTC	120			
DB	19	AAGAGTGTCT	TACAGCAGCTGGCGGAGAGCCGCGATGGCGGGTGGAGGTCTTC	78			
QY	121	TACGATAAGGTGCTGCTGACCCGAGAGTCTGCCCTTTTCGAGTCCCTGGACATGCAA	180				
DB	79	TACCGAAGGTGCTGCGGAGCATCATCAGCCACTTCTTCGAGGACGTGGACATGGAG	138				
QY	181	GACGAGAGTGAAGCAGGTCAAGTTTCATGAGCTTTCGTTTTCGCGGAGCAGACCAATAC	240				
DB	139	CGCCAGCGCCGGAAGCAGAGGCGGTTCCTTGACATGGTGGCGGTGGCGCGGTCCATC	198				
QY	241	AAGGGCGGAAGCATGTACGACGACGACCATCTGTGTCAAGGGCCACGCGCTGGACCA	300				
DB	199	TCGGGAGAGCATGCGCGGCGGACCGGCTCTGTGTGAAG---	255				
QY	301	CGCCACTTTGACAAAGATCAAGCAGTACCTTTGGAGAGACGCTGCAAGAGATGGCGCTCA	360				
DB	256	TCGCACTTCGACGCGGTGGCGGCGCCCTGAAGCGACGCTGGAGGAGCTGGCGCTGCC	315				
QY	361	CAGGATGTGATCCAGCACGCGCGGAGTGGTGGAGTCCACCCGCGGACGA	410				
DB	316	GCGCCGCTGTTGGCGGAGGTGATGACCATCGCGGAGAGCGCCCGCGCGGA	365				

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US-09-902-540-1273
; Sequence 1273, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1273
; LENGTH: 72704
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(72704)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1273

Query Match      16.3%; Score 97.2; DB 4; Length 72704;
Best Local Similarity 56.9%; Pred. No. 2e-16;
Matches 199; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

QY 61 AAGAGCTGTTTGTGACCTGGCGCGCAGAGGATGAAGCTGGCGGTGACACCTTC 120
DB 21785 AAGAGTGTCTACGACAGCTGGCGGAGAGCCGCGGATGGCGCGGTGGAGTCTTC 21844

QY 121 TAGCATAGTGTGCTGACCGGAGCTGCTGCCCTTCTTCGAGTCCCTGGACATGCAA 180
DB 21845 TACCGAAGTGTCTGGCGAGCATCACATCAGCCACTTCTTCGAGGAGCTGGACATGAG 21904

QY 181 GAGCAGAGATGAAGAGTGAAGTTCATGACTTCGTTGTTGGCGGAGCAGACCAATAC 240
DB 21905 CGCCAGCGCCGAGCAGAGGCGTTCCTGACATGGTGAACGGTGGCGCGGTCCACTAC 21964

QY 241 AAGGCGGAGGATGTACACACGACGACGCTGCTGTTCAAGGCGCAGCGCTGGACAC 300
DB 21965 TCGGCAAGGACATGCGCGCGGCGCACGCGCTCTGGTGAAG--CGTGGGTGAACGAC 22021

QY 301 CGCCACTTTGACAAGATCAAGCAGTACCTTTGAGAGACGCTGCAAGAGATGGCGTCAAG 360
DB 22022 TCGCACTTCAGCGGTGGCGGCGCACCTGAAGGCGACGCTGGAGGAGCTGGCGGTGGCC 22081

QY 361 CAGGATGTATCAGACACCGCGCGGAGTGGTGGAGTCCACCGCGCAGA 410
DB 22082 GCGCGCTGTTGGCGGAGGTGATGACCATCGCGGAGAGCGCGCGCGGA 22131

RESULT 3
US-09-103-840A-2/c
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2

Query Match      7.8%; Score 46.4; DB 3; Length 4411529;
Best Local Similarity 50.9%; Pred. No. 0.11;
Matches 110; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 51 ATCGGGCGCGCAAGAAGCTGTTTGTGATGACCTGGCGCGCAGAGGATGAAGCTGGCGGT 110
DB 1744808 ACGTGAGCCGATCAGCATCTACGACAAGATCGCGGGCATGAGCCATCGAAGTCGTCT 1744749

QY 111 TGACACCTTCTACGATAAGTGTGGTGTGACCCCGAGCTGCTGCCCTTCTTCGAGTCCCT 170
DB 1744748 CGAGGACTTCTATGTTGCTGTGCTTGCATGACCAACTATCGGCTTCTTCAGCGGTAC 1744689

QY 171 GGACATGCAAGCAGCAGAGATGAAGCAGGTCAAGTTCATGAGCTTCGTTGTTGGCGGAGC 230
DB 1744688 GAACATGAGCCGCTCAAGGGCAAGCAGGTGGAGTTTTTCGCGCGCGCTTGGCGGCC 1744629

QY 231 AGACCAATACAAGGGCGCGAAGCATGTACAGCGCACA 266
DB 1744628 CGAGCCCTATACCGTGGCGCGCATGAAGCAAGTCCA 1744593

; SEQ ID NO 2
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LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match      7.8%; Score 46.4; DB 3; Length 4403765;
Best Local Similarity 50.9%; Pred. No. 0.11;
Matches 110; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 51 ATCGGGCGCGCAAGAAGCTGTTTGTGATGACCTGGCGCGCAGAGGATGAAGCTGGCGGT 110
DB 1744933 ACGTGAGCCGATCAGCATCTACGACAAGATCGCGGGCATGAGCCATCGAAGTCGTCT 1744874

QY 111 TGACACCTTCTACGATAAGTGTGGTGTGACCCCGAGCTGCTGCCCTTCTTCGAGTCCCT 170
DB 1744873 CGAGGACTTCTATGTTGCTGTGCTTGCATGACCAACTATCGGCTTCTTCAGCGGTAC 1744814

QY 171 GGACATGCAAGCAGCAGAGATGAAGCAGGTCAAGTTCATGAGCTTCGTTGTTGGCGGAGC 230
DB 1744813 GAACATGAGCCGCTCAAGGGCAAGCAGGTGGAGTTTTTCGCGCGCGCTTGGCGGCC 1744754

QY 231 AGACCAATACAAGGGCGCGAAGCATGTACAGCGCACA 266
DB 1744753 CGAGCCCTATACCGTGGCGCGCATGAAGCAAGTCCA 1744718

RESULT 4
US-09-103-840A-1/c
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1

Query Match      7.8%; Score 46.4; DB 3; Length 4411529;
Best Local Similarity 50.9%; Pred. No. 0.11;
Matches 110; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

QY 51 ATCGGGCGCGCAAGAAGCTGTTTGTGATGACCTGGCGCGCAGAGGATGAAGCTGGCGGT 110
DB 1744808 ACGTGAGCCGATCAGCATCTACGACAAGATCGCGGGCATGAGCCATCGAAGTCGTCT 1744749

QY 111 TGACACCTTCTACGATAAGTGTGGTGTGACCCCGAGCTGCTGCCCTTCTTCGAGTCCCT 170
DB 1744748 CGAGGACTTCTATGTTGCTGTGCTTGCATGACCAACTATCGGCTTCTTCAGCGGTAC 1744689

QY 171 GGACATGCAAGCAGCAGAGATGAAGCAGGTCAAGTTCATGAGCTTCGTTGTTGGCGGAGC 230
DB 1744688 GAACATGAGCCGCTCAAGGGCAAGCAGGTGGAGTTTTTCGCGCGCGCTTGGCGGCC 1744629

QY 231 AGACCAATACAAGGGCGCGAAGCATGTACAGCGCACA 266
DB 1744628 CGAGCCCTATACCGTGGCGCGCATGAAGCAAGTCCA 1744593

; SEQ ID NO 1
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RESULT 5
US-09-902-540-8600
; Sequence 8600, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 8600
; LENGTH: 1143
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-8600

Query Match      7.6%; Score 45.2; DB 4; Length 1143;
Best Local Similarity 45.5%; Pred. No. 0.011;
Matches 158; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

QY 82 GCGCGCGCAGAAGCATGAAGCTGGCGGTTGACACCTTCTACGATGAAGTGTGGCTGAC 141
Db 169 GGGCTGCTCGCGCGCGGCGCTGGCGACGTGTGTTCCACGACGCGCCCTGTCAACGC 228
QY 142 CCGGAGCTGCTGCCCTTCTTCGAGTCCCTGGACATCAAGAGAGATGAAGCAGGTC 201
Db 229 TCGCGCACGGTGTCTCGCGAGCTGCCATGGCGGAGGCGCTGACGTTGCCACCGCC 288
QY 202 AAGTTTCATGAGCTTCTGTTTGGCGGAGCAGACCATCAAGAGAGATGAAGCAGGTC 261
Db 289 AAGCCCAAGGCTCGGACGCGACCTGTCCGAGGCGCAACCGCCACCTGTGTAACGTC 348
QY 262 GCACAGCCCATCTGTTTGGCGGAGCAGACCAATACAAAGGCGCGCAAGCATGTACGAC 321
Db 349 GCCTACAAACGCTGTTTCATGTGGAGCGGACCGGCGGAGCGGCTCTGGAACACGCGCATC 408
QY 322 CAGTACCTTGGAGAGCTGCAAGAGATGGCGTCAAGCAGGATGTATCCAGCAGCC 381
Db 409 CTGCGCTGTCTCAACCGGTTGAGATGAACCGGACCGCAGGTGTGCGCGCCGCTC 468
QY 382 GCGGAGTGTGGAGTCCACCGCGAGCAATTTGACTTNCACAA 428
Db 469 ACCTCGTGGAGTGTACACACCGAGTACCGAGGCCCTCTTTCGGCAA 515

RESULT 6
US-09-902-540-907
; Sequence 907, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 907
; LENGTH: 6821
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:

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; NAME/KEY: unsure
; LOCATION: (1)..(6821)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-907

Query Match      7.6%; Score 45.2; DB 4; Length 6821;
Best Local Similarity 45.5%; Pred. No. 0.021;
Matches 158; Conservative 0; Mismatches 189; Indels 0; Gaps 0;

QY 82 GCGCGCGCAGAAGCATGAAGCTGGCGGTTGACACCTTCTACGATGAAGTGTGGCTGAC 141
Db 5097 GGGCTGCTCGCGCGCGGCGCTGGCGACGTGTGTTCCACGACGCGCCCTGTCAACGC 5156
QY 142 CCGGAGCTGCTGCCCTTCTTCGAGTCCCTGGACATCAAGAGAGATGAAGCAGGTC 201
Db 5157 TCGCGCACGGTGTCTCGCGAGCTGCCATGGCGGAGGCGCTGACGTTGCCACCGCC 5216
QY 202 AAGTTTCATGAGCTTCTGTTTGGCGGAGCAGACCATCAAGAGAGATGAAGCAGGTC 261
Db 5217 AAGCCCAAGGCTGCGACGACACCTGTCCGAGCGCAACCGCCACCTGTGTAACGTC 5276
QY 262 GCACAGCCCATCTGTTTGGCGGAGCAGACCATCAAGAGAGATGAAGCAGGTC 321
Db 5277 GCTTACAAACGCTGTTTCATGTGGAGCGGACCGGCTCTGGAACGAGGCGCATC 5336
QY 322 CAGTACCTTGGAGAGCTGCAAGAGATGGCGTCAAGCAGGATGTATCCAGCAGCC 381
Db 5337 CTGCGCTGTCTCAACCGGTTGAGATGAACCGGACCGCAGGTGTGCGCGCCGCTC 5396
QY 382 GCGGAGTGTGGAGTCCACCGCGAGCAATTTGACTTNCACAA 428
Db 5397 ACCTCGTGGAGTGTACACACCGAGTACCGAGGCCCTCTTTCGGCAA 5443

RESULT 7
US-09-902-540-14/c
; Sequence 14, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 14
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(603)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-14

Query Match      7.3%; Score 43.4; DB 4; Length 603;
Best Local Similarity 45.4%; Pred. No. 0.026;
Matches 152; Conservative 0; Mismatches 183; Indels 0; Gaps 0;

QY 30 CACAGACCGCGGAGCGGATCGCGGCGCAAGAACTGTTTCATGACCTGGCGGCGC 89
Db 601 CGCAATATCCCGGCGGCGGATCGCGGCGCAAGAACTGTTTCATGACCTGGCGGCGC 542
QY 90 AGAAGGCATGAAGCTGGCGGTTGACACCTTCTACGATAAGGTGTGCTGACCGGAGCT 149
Db 541 GCTCAACCGCGGAGCTGTCTACCGGACCGCGGCGGCGGAGGTGTGCTCGCGCATC 482
QY 150 GCTGCCCTTCTTCGAGTCCCTGGACATGCAAGAGCAGAGATGAAGCAGGTCATTCAT 209

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Fri Feb 25 16:26:58 2005

481 TGGCCCTTCGCCAAGTAGCTGGGCGGCTGGAGCTGGTGTGAAGATGCCCGAGGTGCT 422
210 GAGCTTCGTGTTGGCGGAGCAGACCAATACAAAGGCGGAGCATGTACGACGACACGC 269
421 CGGACCCGCTGAGGCGCGGAAATCATCAGCCAGGACTTACCGCGTGTTCGCCATGGACGC 362
270 CCATCTGTCAAGGCCAGCGGCTGGACCGCCACTTTGACAAAGATCAAGCAGTACCT 329
361 CCTGTGGTGCAGCAGCGCATGCGCCGTTTCGCCACGACAGCGGTTCCTGGGAGGA 302
330 TCGAGAGACGCTGCAAGAGATGGCGTCAACAGCAGG 364
301 GGGCCAGTTCCTCCGCGAGGAGCGAGTCCGTGAGG 267

RESULT 8
US-09-902-540-5853
; Sequence 5853, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 5853
; LENGTH: 603
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(603)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-5853

Query Match 7.3%; Score 43.4; DB 4; Length 603;
Best Local Similarity 45.4%; Pred. No. 0.026;
Matches 152; Conservative 0; Mismatches 183; Indels 0; Gaps 0;
QY 30 CACAGAGACGCGGAGCGGATCGGGCGCAAGAGCTGTTTGTACCTGGGCGGC 89
DB 3 CGAAATCCCGGNCGTGGTGGCGTGGACNCGGTGATGGTGGCCACCTGCACGTCGT 62
QY 90 AGAAGGCATGAAGCTGGCGGTTGACCTTCTAGGATAAGGTGCTGACCCGAGCT 149
DB 63 GCTCAACCCGCGGAGCTGCTCACCGACCCCGCGGCGCAAGGTGTGCTCGGCATC 122
QY 150 GCTGCCCTTCCTGAGTCCCTGGACATGCAAGACGAGATGAAGCAGTCAAGTTCA 209
DB 123 TGGCGCTTCGCCAAGTACGTGGCGCGTGGAGCTGGTGAAGATGCCCGAGGTGCT 182
QY 210 GAGCTTCCTGTTTGGCGGAGCAGACCAATACAAAGGCGGAGCATGTACGACGACGC 269
DB 183 CGGACCCGTTGAGGCGCGGAAATCATCAGCCAGGACTTACCGCGTGTTCCTCCATGGACGC 242
QY 270 CCATCTGTCAAGGCCAGCGGCTGGACCGCCACTTTGACAAAGATCAAGCAGTACCT 329
DB 243 CCTGTGGTGCAGCAGCGCATGCGCCGTTTCGCCACGACAAACAGCGTTCCTGGGAGGA 302
QY 330 TCGAGAGACGCTGCAAGAGATGGCGTCAACAGCAGG 364
DB 303 GGGCCAGTTCCTCCGCGAGGAGCGAGTCCGTGAGG 267

RESULT 9
US-09-902-540-3555

; Sequence 3555, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 3555
; LENGTH: 585
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; US-09-902-540-3555

Query Match 7.2%; Score 42.8; DB 4; Length 585;
Best Local Similarity 48.4%; Pred. No. 0.038;
Matches 119; Conservative 0; Mismatches 127; Indels 0; Gaps 0;
QY 78 CTTGGCGCGGCGAAGAGCATGAAGCTGGCGGTTGACCTTCTAGCATAGGTGCTGGC 137
DB 18 CGTGGCATCGCGGGCTGCTCCACCTGGGAGACGCGTCTTCTTCGAGCGGATGCCAG 77
QY 138 TGACCCGAGCTGCTGCCCTTCTTCAGTCCCTGGACATGCAAGACGAGCATGAAGCA 197
DB 78 CCAGGCGCAGATGCTGGCGAGCATCGAGAAGCTGGACAAGAGGAGGCCAGACCA 137
QY 198 GGTCAAGTTCATGAGCTTCTGTTTGGCGGAGCAGACCAATACAAAGGCGGAGCATGTA 257
DB 138 GGCTGTCATCAGCAAGTGCAGAGCGCGCGCGGAGCCCGCGAGGACAGCTACGATTG 197
QY 258 CGAGCAGACGCCCATCTGTCAAGGCGGACCGCTGGACCCGACCTTTGACAAGAT 317
DB 198 CTCTGCGGAGCAGTGTGCTGGTGGTGGCGAGCAGACCCCACTCCCGCGTGGAGAGCT 257
QY 318 CAAGCA 323
DB 258 CAAGCA 263

RESULT 10
US-09-902-540-1171
; Sequence 1171, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 1171
; LENGTH: 19019
; TYPE: DNA
; ORGANISM: Myxococcus xanthus
; FEATURE:
; NAME/KEY: unsure
; LOCATION: (1)..(19019)
; OTHER INFORMATION: unsure at all n locations
US-09-902-540-1171

Query Match 7.2%; Score 42.8; DB 4; Length 19019;
Best Local Similarity 48.4%; Pred. No. 0.14;

Matches 119; Conservative 0; Mismatches 127; Indels 0; Gaps 0;

QY 78 CTGGGGGGGCGGAGGATGAGCTGGCGTTGACACCTTCTAGATAAGTGTGGC 137
 Db 9777 CGTGGCGATCGCGGGGTGCTCCACCTGGAGACGGTCTCTTTCGAGCGGATGCCAG 9836

QY 138 TGACCCGGAGCTGCTGCCCTTCTTTCGAGTCCCTGGACATGCAAGACAGAGAATGAAGCA 197
 Db 9837 CCAGGCGGAGATGCTGGCGAGCATCGAGAAGCTGGACAGAAGAGAGAGAGAGAGAGAG 9896

QY 198 GGTCAAGTTATGAGCTGCTGTTTGGCGGAGCAGACCAATATCAAGGGCGGAAGCATGTA 257
 Db 9897 GGCCTGCATCAGCAAGTGCAGAGAGCGCGCGCGGGAGCCCGCGAGGACAGCTTACGATTG 9956

QY 258 CGAGCGACACGCCCATCTGTCTAAGGGCCACCGCTGGACACCGCCACTTTGACAAAGAT 317
 Db 9957 CTCCTGGCGGAGAGTGATGGCTGGCGAGACCCCAACCTCCCGCTCGGAGAGCT 10016

QY 318 CAAGCA 323
 Db 10017 CAAGCA 10022

RESULT 11
 US-09-744-072-1
 ; Sequence 1, Application US/09744072
 ; Patent No. 6823328
 ; GENERAL INFORMATION:
 ; APPLICANT: SCHERER, STEPHEN W.
 ; APPLICANT: MINASSIAN, BERGE A.
 ; APPLICANT: ROULEAU, GUY
 ; APPLICANT: DALGADO-ESCUETA, ANTONIO
 ; TITLE OF INVENTION: LAFORA'S DISEASE GENE
 ; FILE REFERENCE: 086671/0113
 ; CURRENT APPLICATION NUMBER: US/09/744,072
 ; CURRENT FILING DATE: 1999-07-20
 ; PRIOR APPLICATION NUMBER: 60/093,495
 ; PRIOR FILING DATE: 1998-07-20
 ; PRIOR APPLICATION NUMBER: 60/130,269
 ; PRIOR FILING DATE: 1999-04-21
 ; NUMBER OF SEQ ID NOS: 32
 ; SOFTWARE: Patent In Ver. 2.1
 ; SEQ ID NO 1
 ; LENGTH: 3128
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; ORGANISM: Homo sapiens
 ; US-09-744-072-1

Query Match 7.1%; Score 42.6; DB 4; Length 3128;
 Best Local Similarity 50.7%; Pred. No. 0.081;
 Matches 102; Conservative 0; Mismatches 99; Indels 0; Gaps 0;

QY 1 CGCTGCTGCTGAGACGGCGCCACAGCACCAAGAGACGGCGGAGCGGATGCGGGCCG 60
 Db 22 GTGGTCCACCCGCGGTGGCGGGCGCGCGCGCGGAGCTGCTGGTGGTGGGCTGCGGGCC 81

QY 61 AAGAGCTGTTGATGACCTGGCGGGCGGAGAGGATGAGCTGGCGGTTGACACCTTC 120
 Db 82 GAGCTGGGGCGTTGGGAGCGCGCGGTGCGCGTCCGCTGAGCGCGCGCGGACCGCGCGG 141

QY 121 TACGATAAGGTGCTGGCTGACCGCGGAGCTGCTGCGCTTCTTCGAGTCCCTGGACATCAA 180
 Db 142 GCGACCGGGCCCTTGGCGTGCAGAGCGCGGGCTGTGGCTCGGGGAGGTGGAGCTGGG 201

QY 181 GAGCAGAAGATGAAGAGGTC 201
 Db 202 GCCGAGGAGGCGGCGCAGGAC 222

RESULT 12
 US-09-949-016-16800
 ; Sequence 16800, Application US/09949016
 ; Patent No. 6812339

GENERAL INFORMATION:
 ; APPLICANT: VENTER, J. Craig et al.
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
 ; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: CL001307
 ; CURRENT APPLICATION NUMBER: US/09/949,016
 ; CURRENT FILING DATE: 2000-04-14
 ; PRIOR APPLICATION NUMBER: 60/241,755
 ; PRIOR FILING DATE: 2000-10-20
 ; PRIOR APPLICATION NUMBER: 60/237,768
 ; PRIOR FILING DATE: 2000-10-03
 ; PRIOR APPLICATION NUMBER: 60/231,498
 ; PRIOR FILING DATE: 2000-09-08
 ; NUMBER OF SEQ ID NOS: 207012
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 16800
 ; LENGTH: 26896
 ; TYPE: DNA
 ; ORGANISM: Human
 ; ORGANISM: Human
 ; US-09-949-016-16800

Query Match 7.1%; Score 42.4; DB 4; Length 26896;
 Best Local Similarity 47.7%; Pred. No. 0.21;
 Matches 124; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

QY 137 CTGACCCGGAGCTGCTGCCCTTCTTCGAGTCCCTGACATGCAAGACAGAGAAAGATGAAGC 196
 Db 22334 CAGACCATGTGCACCTCTCTCTGCACACAGAGCCGCCATGATGGCAGAGAGCTGAAGA 22393

QY 197 AGTCAAGTTATGAGCTTCTGTTGGGGGAGCAGCAATACAAAGGGCCGAGCATGT 256
 Db 22394 AGGAGCAGGACACACAGCGGCCACCTGGAGCGCATGAAGAAGAAACATGGAAACAGACCATTA 22453

QY 257 AGAGCGCACAGCCCATCTGTCAGGGCCAGCGCTGGACACCGCCACTTTTGACAAGA 316
 Db 22454 AGACCTGCAGCACCGGCTGGACGAAGCCGACAGATCGCCCTCAAGGGCGGCAAGAGC 22513

QY 317 TCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGCTCAAGCAGGATGTGATCCAGC 376
 Db 22514 AGCTGCAGAAAGCTGGAAGCGCGGTGCGGAGATGAGCTGGAGGCGGAGCAGA 22573

QY 377 AGCCCGCGGAGTGTGGAG 396
 Db 22574 AGCGCAACGACAGATCGGTG 22593

RESULT 13
 US-09-252-991A-11092
 ; Sequence 11092, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 11092
 ; LENGTH: 759
 ; TYPE: DNA
 ; ORGANISM: Pseudomonas aeruginosa
 ; ORGANISM: Pseudomonas aeruginosa
 ; US-09-252-991A-11092

Query Match 7.1%; Score 42.2; DB 4; Length 759;
 Best Local Similarity 51.9%; Pred. No. 0.061;
 Matches 95; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

QY 53 GCGGGCGCAAGAAGCTGTTTGTATGACCTGGGCGGCGCAGAGGATGAAGTGGCGGTTG 112

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OM nucleic - nucleic search, using sw model

Run on: February 22, 2005, 20:25:43 ; Search time 402 Seconds
(without alignments)
8792.231 Million cell updates/sec

Title: US-09-920-953-2

Perfect score: 598

Sequence: 1 ggcgtgcctgcagacgcgc.....agccatttcgacccaagcc 598

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 5384158 seqs; 2955248155 residues

Total number of hits satisfying chosen parameters: 10768316

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications NA:

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- 2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
- 3: /cgn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:
- 4: /cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:
- 5: /cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:
- 6: /cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:
- 7: /cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:
- 8: /cgn2_6/ptodata/2/pubpna/US08_PUBCOMB.seq:
- 9: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
- 10: /cgn2_6/ptodata/2/pubpna/US09_PUBCOMB.seq:
- 11: /cgn2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:
- 12: /cgn2_6/ptodata/2/pubpna/US09_NEW_PUB.seq:
- 13: /cgn2_6/ptodata/2/pubpna/US10A_PUBCOMB.seq:
- 14: /cgn2_6/ptodata/2/pubpna/US10B_PUBCOMB.seq:
- 15: /cgn2_6/ptodata/2/pubpna/US10C_PUBCOMB.seq:
- 16: /cgn2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:
- 17: /cgn2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:
- 18: /cgn2_6/ptodata/2/pubpna/US10F_PUBCOMB.seq:
- 19: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:
- 20: /cgn2_6/ptodata/2/pubpna/US11_NEW_PUB.seq:
- 21: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:
- 22: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74.4	12.4	372	17	US-10-282-122A-25335
2	50	8.4	2466	15	US-10-156-761-5788
3	50	8.4	9025608	15	US-10-156-761-1
4	47.6	8.0	2256646	18	US-10-470-565-1
5	47.4	7.9	548	18	US-10-437-963-94550
6	46.6	7.8	1389	18	US-10-411-910A-255
7	46.6	7.8	1389	18	US-10-411-910A-257
8	46.2	7.7	1209	17	US-10-369-493-32038
9	46.2	7.7	1509	18	US-10-411-910A-264
10	45.8	7.7	2209	18	US-10-437-963-69229
11	45.2	7.6	2238	18	US-10-437-963-97363

12	44.4	7.4	1445	18	US-10-437-963-35783
13	44.2	7.4	1000	17	US-10-389-566-49
14	44.2	7.4	1377	17	US-10-369-493-39791
15	44.2	7.4	1395	17	US-10-369-493-39403
16	44.2	7.4	1404	17	US-10-369-493-39036
17	44.2	7.4	2055	17	US-10-389-566-235
18	44	7.4	1368	18	US-10-437-963-7459
19	43.8	7.3	1507	18	US-10-425-115-108376
20	43.8	7.3	2978	18	US-10-739-930-4715
21	43	7.2	681	18	US-10-767-701-23705
22	42.8	7.2	2645	18	US-10-437-963-95877
23	42.6	7.1	1403	15	US-10-156-761-4532
24	42.6	7.1	2121	15	US-10-755-889-419
25	42.6	7.1	3128	18	US-10-156-761-2429
26	42.6	7.1	9025608	15	US-10-886-033-1
27	42.6	7.1	932	18	US-10-156-761-1
28	42.4	7.1	25000	11	US-09-968-007A-215
29	42.4	7.1	1055	18	US-10-437-963-4170
30	42.2	7.0	1058	9	US-09-452-239-11
31	42	7.0	1483	18	US-10-437-963-33390
32	42	7.0	1060	18	US-10-437-963-62449
33	42	7.0	1425	17	US-10-354-437-31
34	41.8	7.0	1280	9	US-09-923-922-4
35	41.6	7.0	1280	9	US-09-954-456-1590
36	41.6	7.0	1280	17	US-10-390-553-4
37	41.6	7.0	1817	9	US-09-924-417-64
38	41.6	7.0	1817	14	US-10-067-741-45
39	41.6	7.0	1817	17	US-10-653-872-64
40	41.6	7.0	2887	15	US-10-327-805-1
41	41.6	7.0	2967	17	US-10-282-122A-14992
42	41.6	7.0	3083	9	US-09-371-900-36
43	41.6	7.0	3083	9	US-09-924-417-62
44	41.6	7.0	3083	9	US-09-970-820-36
45	41.6	7.0	3083	9	US-09-970-820-36

ALIGNMENTS

RESULT 1
US-10-282-122A-25335
Sequence 25335, Application US/10282122A
Publication No. US20040029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELITRA.034A
CURRENT APPLICATION NUMBER: US/10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-09-06
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625

Sequence 35783, A
Sequence 49, Appl
Sequence 39791, A
Sequence 39403, A
Sequence 39036, A
Sequence 235, App
Sequence 7459, Ap
Sequence 108376,
Sequence 4715, Ap
Sequence 23705, A
Sequence 95877, A
Sequence 4532, Ap
Sequence 419, App
Sequence 2429, Ap
Sequence 1, Appli
Sequence 1, Appli
Sequence 5556, Ap
Sequence 215, App
Sequence 4170, Ap
Sequence 11, Appl
Sequence 62449, A
Sequence 33390, A
Sequence 31, Appl
Sequence 4, Appli
Sequence 1590, Ap
Sequence 4, Appli
Sequence 64, Appl
Sequence 45, Appl
Sequence 64, Appl
Sequence 1, Appli
Sequence 14992, A
Sequence 36, Appl
Sequence 62, Appl
Sequence 36, Appl

PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 25335
 LENGTH: 372
 TYPE: DNA
 ORGANISM: Legionella pneumophila
 US-10-282-122A-25335

Query Match 12.4%; Score 74.4; DB 17; Length 372;
 Best Local Similarity 54.0%; Pred. No. 4.9e-13; Indels 3; Gaps 1;
 Matches 175; Conservative 0; Mismatches 146;

QY 68 TGTTCATGACCTGGCGCGCAGAGGATGAGCTGGCGGTGACACCTTCTACGATA 127
 DB 14 TGTTCATGACCTGGCGCGCAGAGGATGAGCTGGCGGTGACACCTTCTACGATA 73
 QY 128 AGGTGCTGGCTGACCGCGAGCTGCTGCCCTTCTTCGAGTCCCTGACATGCAAGACAGA 187
 DB 74 AAATGCTCATGATGACAGATGAATATTTTTCGATGACGTGATATGGAGCAACAA 133
 QY 188 AGATGAGCAGGTCAAGTTTCATGAGCTTCGTTGGCGGAGCAGACCAATACAGAGGCC 247
 DB 134 TCCTTAAGCAAAAGAGATTTTAAACATGCTGTTTGGCGGAGCAATCAATACATGGA 193
 QY 248 GAAGCATGTACGACGACACAGCCCATCTGTTCAAGGGCCACCGCTTGACACACCGCCACT 307
 DB 194 AAGATGTCGGGAGGACATCAGCATCTACT--TGCCAGAGCTTAATGACTCAGATG 250
 QY 308 TTGACAGATCAAGCAGTACCTTGGAGACGCTGCAAGAGATGGCGTCAAGCAGGATG 367
 DB 251 TGGATATTGTAATCGAGCATTTAGGGGAAACCCCTTAAGGAATTTGGCGCCCAATGAGAGG 310
 QY 368 TGATCCAGCAGCGCGCGGAGTGG 391
 DB 311 ACATTAGAAGTAGTGCATCG 334

RESULT 2
 US-10-156-761-5788
 Sequence 5788, Application US/10156761
 Publication No. US20030119018A1
 GENERAL INFORMATION:
 APPLICANT: OMURA, SATOSHI
 APPLICANT: IKEDA, HARUO
 APPLICANT: ISHIKAWA, JUN
 APPLICANT: HORIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHIYUKI
 APPLICANT: HATTORI, MASAHIRA
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-262
 CURRENT FILING DATE: 2002-05-29
 PRIOR APPLICATION NUMBER: US/10/156,761
 PRIOR FILING DATE: 2002-05-29
 PRIOR APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-08-02
 NUMBER OF SEQ ID NOS: 15109
 SEQ ID NO 5788
 LENGTH: 2466
 TYPE: DNA
 ORGANISM: Streptomyces avermitilis
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1)..(2466)

US-10-156-761-5788

Query Match 8.4%; Score 50; DB 15; Length 2466;
 Best Local Similarity 47.1%; Pred. No. 4.6e-05;
 Matches 152; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

QY 115 ACCTTCTAGATAAGTGTGCTGACCCGGAGCTGCTCCCTTCTTCGAGTCCCTGGAC 174
 DB 421 ACCTCCACCTGCTGCTGCCGAGACCCGGCGCTGCTCGCGGAGCGCCCGCTGGTC 480
 QY 175 ATGCAAGAGCAGAAGATGAAGCAGGTCAAGTTCATGAGTTCGTTTTCGCGGAGCAGAC 234
 DB 481 CTGTCGAGCAGAGTTCCTCCACCGCAACAGGTCTCTCAACACCATCCGCGACCTGCAC 540
 QY 235 CAATACAGGCGCCGAGCATGTACGACGACACACCGCCCATCTGTCAGGCGCCACGCGCTG 294
 DB 541 GAGCGCTATCCGCGCGCGGTACGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 600
 QY 295 GACCACCGCACCTTTCACCAAGATCAAGCAGTACCTTTGGAGAGAGCGCTGCAAGAGATGGGC 354
 DB 601 GACCTCGGGCGCTTGGACGAGTTCGCGCGGAGATCGTGCCCGGTGGACCTGATCAGC 660
 QY 355 GTCAAGCAGATGTGATCCAGCAGCGCGCGGAGTGTGAGTTCACCGCGGAGATTT 414
 DB 661 GCGCCTCGGGGACGCTGAGCTGCGCGGCGCTGCTGGAGAAAGGGGAGGAGCTGGTC 720
 QY 415 GACTTNCACCAACTGCGCAC 437
 DB 721 GCGCGCAGGAGGCGCGTACC 743

RESULT 3
 US-10-156-761-1
 Sequence 1, Application US/10156761
 Publication No. US20030119018A1
 GENERAL INFORMATION:
 APPLICANT: OMURA, SATOSHI
 APPLICANT: IKEDA, HARUO
 APPLICANT: ISHIKAWA, JUN
 APPLICANT: HORIKAWA, HIROSHI
 APPLICANT: SHIBA, TADAYOSHI
 APPLICANT: SAKAKI, YOSHIYUKI
 APPLICANT: HATTORI, MASAHIRA
 TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
 FILE REFERENCE: 249-262
 CURRENT FILING DATE: 2002-05-29
 PRIOR APPLICATION NUMBER: US/10/156,761
 PRIOR FILING DATE: 2002-05-29
 PRIOR APPLICATION NUMBER: JP 2001-204089
 PRIOR FILING DATE: 2001-05-30
 PRIOR APPLICATION NUMBER: JP 2001-272697
 PRIOR FILING DATE: 2001-08-02
 NUMBER OF SEQ ID NOS: 15109
 SEQ ID NO 1
 LENGTH: 9025608
 TYPE: DNA
 ORGANISM: Streptomyces avermitilis
 FEATURE:
 NAME/KEY: misc feature
 LOCATION: (418715)
 OTHER INFORMATION: a, t, c, g, other or unknown
 US-10-156-761-1

Query Match 8.4%; Score 50; DB 15; Length 9025608;
 Best Local Similarity 47.1%; Pred. No. 0.00058;
 Matches 152; Conservative 0; Mismatches 171; Indels 0; Gaps 0;

QY 115 ACCTTCTAGATAAGTGTGCTGACCCGGAGCTGCTCCCTTCTTCGAGTCCCTGGAC 174
 DB 7015347 ACCTCCACCTGCTGCTGCCGAGACCCCGGCGCTGCTGGGAGGAGCGCCCGCTGGTC 7015406
 QY 175 ATGCAAGAGCAGAAGATGAAGCAGGTCAAGTTCATGAGCTTCGTTTTCGCGGAGCAGAC 234
 DB 7015407 CTGTCGAGCAGAGTTCCTCCACCGCAACAGCGGTCTCAACACCATCCGCGACCTGCAC 7015466

QY 235 CAATACAGGCGGAGCATGTACGACGACACGCGCCCATCTGCTCAAGGCGCACGCGCTG 294
 Db 7015467 GAGCGTATCCGCGCGCGGCGGTACGTCGTCGCTCGTGGACATGCGCTCCCGGCC 7015526
 QY 295 GACCAACGCGCATCTTTGACAGATCAAGCAGTACCTTTGGAGAGACGCTGCAAGAGATGGCG 354
 Db 7015527 GACCTCGGCGCGCTGACGAGTTTCGCGCGGAGATCGGTGCGCGGTGGACCTGTATCAG 7015586
 QY 355 GTCAAGCAGATGTATTCAGACGCGCGCGGAGTGTGGAGTCCACCCGCGACGAAATT 414
 Db 7015587 GCGCGCTCGGCGCGGTGAGCTGCGCGAGGCGGTGCTGGAGAGGCGGAGGAGCTGGTC 7015646
 QY 415 GACTTCCCAACAACTGCGCAC 437
 Db 7015647 GCCCGGACGAGAGGCGCGTACC 7015669

RESULT 4

US-10-470-565-1/c
 ; Sequence 1, Application US/10470565
 ; Publication No. US20040126870A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Societe des Produits Nestle S.A.
 ; TITLE OF INVENTION: NCC2705 - the genome of a Bifidobacterium
 ; FILE REFERENCE: 80290/WO
 ; CURRENT APPLICATION NUMBER: US/10/470,565
 ; CURRENT FILING DATE: 2003-07-29
 ; PRIOR APPLICATION NUMBER: EP 01102050.0
 ; PRIOR FILING DATE: 2001-01-30
 ; NUMBER OF SEQ ID NOS: 2
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 2256646
 ; TYPE: DNA
 ; ORGANISM: Bifidobacterium longum
 US-10-470-565-1

Query Match 8.0%; Score 47.6; DB 18; Length 2256646;
 Best Local Similarity 44.6%; Pred. No. 0.0022;
 Matches 185; Conservative 0; Mismatches 230; Indels 0; Gaps 0;
 QY 15 CGCGGCGCACGACGACGACGAGCGGCGGAGCGGGATGCGGCGCAAGAAGCTGTTGA 74
 Db 1432814 CGTCTCTACTTACCCGCGCATGGCGTATGAGTGCCACAGGCCAACCCCAAGACGT 1432755
 QY 75 TGACCTGGGCGCGCAGAGGCGATGAAGCTGGCGGTTGACACCTTTCTACGATAGGTGCT 134
 Db 1432754 CGATGAGAACGACCTGTGCGGTCTGTAACGTTGCGGTGAGACCGGACCGCTCGAGGAAGA 1432695
 QY 135 GCGTGACCGGAGCTGCTGCGCTTCTTCGAGTCCCTGGACATGCAAGAGCAGAGATGAA 194
 Db 1432694 GGCCATCAACAGAACCGCCCAAGCAGTGAAGGCGGACGCGGAAGAAACATCACCATCCA 1432635
 QY 195 GCAGGTCAAGTTCATGAGTCTGTTGTTGGCGGAGCAGACCAATACAAAGGCGCGAAGCAT 254
 Db 1432634 GTCCTCAAGCAGCAGACCGACCGCACACCGCTGTGTGACCGGCAAGCGCGACGTCTT 1432575
 QY 255 GTACGACGCGCACCGCCCATCTGTTCAGGCGCGACGCGCTGGACACCGCCCATTTGACAA 314
 Db 1432574 CTTGCGCGATTCCCGGTTGTGCGCTAGCCATCGCCAGACCGATGCTCAGCTGGAACA 1432515
 QY 315 GATCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGTCAAGCAGAGTGTATCCA 374
 Db 1432514 GCTCGGAAGGACTTCGATGAAGTSCCGAAGCGCCATCGCCATCAAGAAAGGCGCATCCCA 1432455
 QY 375 GCACGCGCGGAGTGTGGAGTCCACCGCGGACGAATTTGACTTNCCTCCACACAC 429
 Db 1432454 GACCACCGAAGCGGTGAGAAAGGCCATGCAAAAGCTCATGACGACGCGACCTTAC 1432400

RESULT 5

US-10-437-963-94550

; Sequence 94550, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 94550
 ; LENGTH: 548
 ; TYPE: DNA
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_9282C.1
 US-10-437-963-94550
 Query Match 7.9%; Score 47.4; DB 18; Length 548;
 Best Local Similarity 50.4%; Pred. No. 0.00019;
 Matches 114; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
 QY 216 CGTGTGTTGGCGAGCAGCAATACAAAGGCGGAGCAGTGTAGCAGCAGCAGCCCATCT 275
 Db 194 CGTGTGTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 253
 QY 276 GGTCAAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 335
 Db 254 CGTCATGCTCCACATGCTCAACTTACGAGGCGGTGACCATGACGAGCGCGCGGGA 313
 QY 336 GAGCTGCAAGAGATGGCGGTCAAGCAGGATGTGATCCAGCAGCAGCGCGCGGAGTGTGGA 395
 Db 314 GAGCTCTTCAGAGTCTCGACATGTACGAGGCCACCGCGGCGGCGGCGGCGGCGGCGG 373
 QY 396 GTCACCGCGGAGCAATTTGACTTNCCTCAACAACTGGCAGCCCAAC 441
 Db 374 CGGCTTCTCACCGCGGAGCAGCGGCAACAAACAGCAGCGCGCGCTGACC 419

RESULT 6

US-10-411-910A-255
 ; Sequence 255, Application US/10411910A
 ; Publication No. US20040209256A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Dillon, Harrison F.
 ; TITLE OF INVENTION: Methods and Compositions for Evolving Hydrogenase Genes
 ; FILE REFERENCE: H2041203-P
 ; CURRENT APPLICATION NUMBER: US/10/411,910A
 ; CURRENT FILING DATE: 2003-04-12
 ; NUMBER OF SEQ ID NOS: 343
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 255
 ; LENGTH: 1389
 ; TYPE: DNA
 ; ORGANISM: Mus musculus
 US-10-411-910A-255

Query Match 7.8%; Score 46.6; DB 18; Length 1389;
 Best Local Similarity 44.9%; Pred. No. 0.00046;
 Matches 175; Conservative 0; Mismatches 215; Indels 0; Gaps 0;
 QY 40 GCGGAGCGGAGTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 99
 Db 685 GTGGTGTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCG 744
 QY 100 AAGCTGGCGGTGACACCTTTCTACGATAAGGTGCTGGCTGACCGGAGCTGCTCCCTTC 159

Query Match	7.8%;	Score 46.6;	DB 18;	Length 1389;
Best Local Similarity	44.9%;	Pred. No. 0.00046;		
Matches 175; Conservative	0;	Mismatches 215;	Indels	0; Gaps 0;

QY	40	GCGGACGGGATCGCGGCGCAAGCTGTTTTATCACCCTGGGCGCGCAGAAAGCATG	99
Db	685	GTGGTGTTGCCCCCTGCTACGACAAGACTGGAGGCCCTTCGCAGGGCCCTGAGCAC	744
QY	100	AAGCTGCGGTTGAACCTTCTACGATAAAGTGTCTGGTGTAACCGGAGCTGCTGCCCTTC	159
Db	745	ACCCTGAACGGCGCGCGGACCGACTGTCGTGTGACACGGCGGAGATGCCCCAGATC	804
QY	160	TTCAGTCCCTGGACATGCAAGACGAGAAGATGAAGCAGGTCAAAGTTTCATGAGCTTCGTG	219
Db	805	ATGAGCAGACGACGACCTGAGCGTGAAGGACATCCGCCGTGGACACCCCTGTCGGGACATG	864
QY	220	TTTTGGCGAGCAGACCAATACAAGGGCGCAAGCATGTACGACGACACGCCCATCTGGTC	279
Db	865	AAGAGTGTGCCGTCGACGCGCCACGACGGCGGTGAGCAGCGCACCTGGGCCACATG	924
QY	280	AAGGGCCA CGGCTGGACCA CCGGCCA CTTTGACAAGATCAAGCAGTACCTTTGGAGAGACG	339
Db	925	TTCCGCCACCGCGGCCAAGGAGCTGTTCGGCGAGCACGTGGAGGAGATCACCTACCGGCC	984
QY	340	CTGCAAGAGATGGGCGTCAAGCAGATGTGATCCAGCACCGCGCGGAGTGGTAGAGTCC	399
Db	985	CTGCGCAACAAGGACTTCCAGAGTGAACCTTGGAGAAGACGGCGAGTGCTGTCGGC	1044
QY	400	ACCGCGCAGAAATTGACTTNCCCCAACAC	429
Db	1045	TTCCGCGCGCGCTACCGGCTTCGGCAACATC	1074

	Query Match	7.7%	Score 46.2;	DB 17;	Length 1209;
	Best Local Similarity	55.2%;	Pred. No. 0.00059;		
	Matches	90;	Conservative	0; Mismatches	73; Indels
				0; Gaps	0;
QY	248	GAACATGTCAGGACGACACGCGCCATCTCGTCAAGGGCCACGGCTGGACACCGCCACT	307		
Db	86	GCACCTTGCTTTCGACGAAGTGCTGTGGTGGAGCGCCCGCAGGAGGACGACCTGT	145		
QY	308	TTGCAAGATCAAGACAGTACTCTTGGAGAGACGCTGCAAGAGATGGCGCTCAAGCAGGATG	367		
Db	146	TCGTTCAGCTCTCTCGGGACCGGGGGTGACCGTGATGAATCGGCACCTGCTCGCGG	205		
QY	368	TGATCCAGCACGCGCGCGGAGTGGTGGAGTCCACCGCGCAGCA	410		
Db	206	AGATCTTGCAATCCCGAGGCGCAAGAGTTTATCTCTCGACGA	248		

	Query Match	7.7%	Score 46.2;	DB 18;	Length 1509;
	Best Local Similarity	46.2%;	Pred. No. 0.00064;		
	Matches 153;	Conservative	0;	Mismatches 178;	Indels 0; Gaps 0;
Qy	54	CGGGCGCAGAACTGTTTCATCACCTGGCGCGCAGAGGATGAAGCTGGCGGTTGA	113		
Db	846	CGGCGCGCAGCGCTGCGCGCAGACAAGATCGCCCTCGACAGCAGCCTGGCGCGCGG	905		
Qy	114	CACCTTCTAGATAAGTGCTGGCTACCGCGGAGCTGCTGCCCTTCTTCAGAGTCCCTCGA	173		
Db	906	CGGCGAGATCGCCAGATCATGAGCAGGCGACCTGAGGTGGCGCAACGCCGCGGTGA	965		

QY 174 CATCAAGAGCAGAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTGTTTGGCGGAGCAGA 233
Db 966 CACCTTGTTCGGGACCTGAGAGGAGCAAGGTGACCCGCCACGACGGCGCCAGCAGCGA 1025
QY 234 CCAATACAAGGGCCGAGCATGTACGACGACGCCCCATCTGGTCAAGGGCCACGGCCT 293
Db 1026 CGGCCACCTGGCCACATCTTCGCCACGCGCCCAAGGAGCTGTTCACAGGAGACGTGA 1085
QY 294 GGACACCCGCCATTTGACAAGATCAAGCAGTACCTTGGAGAGAGCGCTCAAGAGATGG 353
Db 1086 GGAGGTGACCTACCGCGCCCTCGCAACAAGGACTTCCAGGAGGTACCCCTGGAGAGAA 1145
QY 354 CGTCAAGCAGGATGTATCCAGCAGCGCCGCC 384
Db 1146 CGCGAGGTGGTCTCGCTTCGCCGCCGCC 1176

RESULT 10
US-10-437-963-69229
; Sequence 69229, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 69229
; LENGTH: 2209
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_69918C.1
US-10-437-963-69229

Query Match 7.7%; Score 45.8; DB 18; Length 2209;
Best Local Similarity 46.1%; Pred. No. 0.00096;
Matches 152; Conservative 0; Mismatches 178; Indels 0; Gaps 0;
QY 110 TTGACACCTCTACGATAAGGTGCTGGCTCACCGGAGCTGTGCCCTTCTTCGAGTCCC 169
Db 400 TCGACTACGTGTGCTCAAGCGGACCGACCGCGGAGCTCCCGGAGCTGTGGCGG 459
QY 170 TGGACATCAAGAGCAGAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTGTTTGGCGGAG 229
Db 460 AGATCATCCAGCGGAACAAGCTGTGGGCTGGAGGAGTACAAGTTCTCTCAAGGTCA 519
QY 230 CAGACCAATACAAGGGCCGAAGATGTACGACGACACGCCCTCTGGTCAAGGGCCACG 289
Db 520 TCGTCAACTCCGGCATCCGGGAGGAGACCTACGGGCGCCGGAACATCATCGCGCGGCG 579
QY 290 GCCTGGACACCGCCACTTTGACAAGATCAAGCAGTACCTTGGAGAGACCTGCAAGAGA 349
Db 580 ACGCCGCCCGCGCCGCTCGCGAGGGGATGGAGGAGATGGAGCAGACGTTCACGCCG 639
QY 350 TGGCGGTCAAGCAGGATGTATCCAGCAGCAGCGCGCGGAGTGGTGGAGTCCACCGCGAAG 409
Db 640 TGCTCAGCAGGTGTTTCGCGGCTCTGTCGCGGGCGGGCGGGCGGTTCGCCCGCG 699
QY 410 AATTGACTTNCACCAACATGCGCACCCA 439
Db 700 ACGTCGACCTCTCGTCTCAACGTGTCCA 729

RESULT 11
US-10-437-963-97363/c
; Sequence 97363, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 97363
; LENGTH: 2238
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_95374C.1
US-10-437-963-97363

Query Match 7.6%; Score 45.2; DB 18; Length 2238;
Best Local Similarity 50.2%; Pred. No. 0.0015;
Matches 110; Conservative 0; Mismatches 109; Indels 0; Gaps 0;
QY 216 CGTGTTCGGGAGCAGACCAATACAAAGGCGCGAAGCATGTACGACGACACGCCCATCT 275
Db 1249 CGTGTTCGGGCTGCGACGCGCGCTCGCGCGCATCTTCGTGACCTCGCCGCTG 1190
QY 276 GGTCAAGGGCCACGGCTGGACCAACCGCCACTTTGACAGATCAAGCAGTACCTTGAGA 335
Db 1189 CGCATGCTCCAGATGCTCAACTTACCGAGGCGGTGCGCATGACGAAGCGCCGCCGA 1130
QY 336 GACGCTGCAAGAGATGGGCTCAAGCAGGATGTATCCAGCAGCGCGCGAGTGGTGA 395
Db 1129 GAAGCTTTCAGGTGCTCGACATGTACGAGGCGGTCCGCGACGCGCCCGCTCATCGA 1070
QY 396 GTCACCCCGCGACGAATTTGACTTNCACCAACTCGCG 434
Db 1069 CGCTTCATCGCGCTGCTCCACCAACGAGCGCGCGC 1031

RESULT 12
US-10-437-963-35783
; Sequence 35783, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 35783
; LENGTH: 1445
; TYPE: DNA
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_39672C.1

US-10-437-963-35783

Query Match 7.4%; Score 44.4; DB 18; Length 1445;
 Best Local Similarity 46.5%; Pred. No. 0.0023;
 Matches 141; Conservative 0; Mismatches 162; Indels 0; Gaps 0;

QY 139 GACCCGAGCTGTCGCCCTTCTTCGAGTCCCTGGACATCAAGAGCAGAAAGATGAAGCAG 198
 |||||
 Db 167 GACCGCTCGAGCTGCGCCAGCAGCTCGACCGGAGCTCGCGAGCTCGAGCCCAAGCTG 226
 |||||

QY 199 GTCAAGTTCATGAGCTTCGTGTTGGCGGAGCAGCAATACAAGGCGCGAAGCATGTAC 258
 |||||
 Db 227 GCCCAGCTGCCCGCGCGGCAACCGCGCGTCTGTCAGGTGCAAGCGCTGACAGGAC 286
 |||||

QY 259 GAGCAGACGCCATCTGCTCAAGGCGCAGCGCTGGACACCGGCACCTTTCACAGATC 318
 |||||
 Db 287 GAGCGGTGAGCCACATGCTCATGACCTCTCTCCGCGCCGCGACTGCTCGACTGGATC 346
 |||||

QY 319 AAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGTCAAGCAGATGTGATCCAGCAC 378
 |||||
 Db 347 CGCTCCCGCGCGCGCGCGCTCCCGAGCCCGTCCGCGCGCGTCTCGCGAGCTC 406
 |||||

QY 379 GCGCGGAGTGGTGAAGTCCACCGCGCAGCAATTTGACTTNCACAACTGCGCACCC 438
 |||||
 Db 407 GCGGAGGCGCTCGCGACTGCGCACCGCGCGCGGTGCGCCACCGCGACGTCAAGCCGAC 466
 |||||

QY 439 AAC 441
 |||||
 Db 467 AAC 469

RESULT 13

US-10-389-566-49/c
 ; Sequence 49, Application US/10389566
 ; Publication No. US20040025202A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Monsanto Technology, LLC
 ; APPLICANT: Laurie, Cathy C
 ; TITLE OF INVENTION: Nucleic Acid Molecules Associated with Oil in Plants
 ; FILE REFERENCE: 38-77(52900)D
 ; CURRENT APPLICATION NUMBER: US/10/389,566
 ; CURRENT FILING DATE: 2003-03-31
 ; PRIOR APPLICATION NUMBER: US 60/365,301
 ; PRIOR FILING DATE: 2002-03-15
 ; PRIOR APPLICATION NUMBER: US 60/391,786
 ; PRIOR FILING DATE: 2002-06-25
 ; PRIOR APPLICATION NUMBER: US 60/392,018
 ; PRIOR FILING DATE: 2002-06-26
 ; NUMBER OF SEQ ID NOS: 2459
 ; SOFTWARE: PatentIn version 3.2
 ; SEQ ID NO 49
 ; LENGTH: 1000
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 US-10-389-566-49

Query Match 7.4%; Score 44.2; DB 17; Length 1000;
 Best Local Similarity 53.8%; Pred. No. 0.0024;
 Matches 91; Conservative 0; Mismatches 78; Indels 0; Gaps 0;

QY 66 GCTGTTTATGACCTGGCGCGCAGAGGATGAAGTGGCGGTGACACCTTCTACGA 125
 |||||
 Db 676 GCAGTTTCATCGCGCGGTCCACCGCGCGCGAGATGCTCAGGTAGAGGGTACACGA 617
 |||||

QY 126 TAAGTGTGCTGATCGCCGAGCTGCTGCTTCTTCAGTCCCTGGACATGCAAGACA 185
 |||||
 Db 616 CATCGTGTGCGCGAGGGAAGCCGCTGTCCGCGCGCGAGATCTCTGGGTGACCGCCCC 557
 |||||

QY 186 GAAGATGAAGCAGGTCAAGTTCATGAGTTCGTGTTGGCGGAGCAGAC 234
 |||||
 Db 556 GACGCTCAAGAGTGGAGAGGTGGCGCGCGTGTGTTCTGTCGCGAC 508
 |||||

RESULT 14

US-10-369-493-39791
 ; Sequence 39791, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 39791
 ; LENGTH: 1377
 ; TYPE: DNA
 ; ORGANISM: Xanthomonas campestris
 US-10-369-493-39791

Query Match 7.4%; Score 44.2; DB 17; Length 1377;
 Best Local Similarity 48.2%; Pred. No. 0.0027;
 Matches 124; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 151 CTGCCCTTCTTCGAGTCCCTGGACATGCAAGAGCAGAAAGATGAAGTCAAGTTCATG 210
 |||||
 Db 784 CTGCCCGCTAGGTGGTTCGATGGCGACAGGAGTGTTCAGCCAGCAGGAGTTGCTG 843
 |||||

QY 211 AGCTTCGTGTTGGCGGAGCAGCAATACAAAGGCGCAAGCATGTACGACACGCC 270
 |||||
 Db 844 GACCTGTTTCGACGTCAAGGACGTCAATTCGAAGGCGCGCTGGACATGGCCCAAGCTC 903
 |||||

QY 271 CATCTGTCGAAGGCGCGCTGGACCAACCGCCCACTTTGACAAGATCAAGCAGTACCTT 330
 |||||
 Db 904 GGCTGGTGTATCAGCATTAATTGAAGACCGCAGCCGCGCAGCATCGCGCGAGCTG 963
 |||||

QY 331 GGAGAGACGCTGCAAGAGATGGCGTCAAGCAGAGATGTATCCAGCAGCGCGCGAGTG 390
 |||||
 Db 964 GAATACCAAGTCCGCAAGCTGGCATTTGATGTGGCGCGCGCGCTGCCGATGTG 1023
 |||||

QY 391 GTGGAGTCCACCCGCGA 407
 |||||
 Db 1024 GTGGTGGCTGCGCGA 1040
 |||||

RESULT 15

US-10-369-493-39403
 ; Sequence 39403, Application US/10369493
 ; Publication No. US20030233675A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Hinkle, Gregory J.
 ; APPLICANT: Slater, Steven C.
 ; APPLICANT: Goldman, Barry S.
 ; APPLICANT: Chen, Xianfeng
 ; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
 ; FILE REFERENCE: 38-10(52052)B
 ; CURRENT APPLICATION NUMBER: US/10/369,493
 ; CURRENT FILING DATE: 2003-02-28
 ; PRIOR APPLICATION NUMBER: US 60/360,039
 ; PRIOR FILING DATE: 2002-02-21
 ; NUMBER OF SEQ ID NOS: 47374
 ; SEQ ID NO 39403
 ; LENGTH: 1395
 ; TYPE: DNA
 ; ORGANISM: Xanthomonas campestris
 US-10-369-493-39403

Fri Feb 25 16:26:58 2005

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Query Match      7.4%; Score 44.2; DB 17; Length 1395;
Best Local Similarity 48.2%; Pred. No. 0.0027;
Matches 124; Conservative 0; Mismatches 133; Indels 0; Gaps 0;

QY 151 CTGCCCTTCTCGAGTCCCTGGACATGCAAGAGCAGAGATGAAGCAGGTCAAGTTTCATG 210
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 793 CTGGCCCGCTAGGTTGGTCGATGGCGACCAAGAGCTGTTTCAGCCAGCAGGAGTTGCTG 852

QY 211 AGCTTCGTGTTTGGCGGAGCAGACCAATACAAAGGGCCGAAGCATGTACGACGCACACGCC 270
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 853 GACCTGTTTCGACGTCAAGGACGTCAAATTCGAAGGCCCGCGCTTGACATGGCCAAAGCTC 912

QY 271 CATCTGCTCAAGGGCCACCGCCTGGACACCGCACTTTGACAAAGATCAAGCAGTACCTT 330
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 913 GGCTGGGTGAATCAGCATTAATTGAAGACCGACCGCCGCGCATCGCGCCGAGCTG 972

QY 331 GGAGAGACGTGCAAGAGATGGCGCTCAAGCAGGATGTGATCCAGCAGCCGCCCGGAGTG 390
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 973 GAATACCAAGCTCCGCAAGCTGGGCATTGATGTGGCCGCCGCCGCCCGCTGCCGATGTG 1032

QY 391 GTGGAGTCCACCCGCGA 407
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1033 GTGGTGGCGCTGCGCGA 1049
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Search completed: February 22, 2005, 21:21:44
Job time : 425 secs

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OM nucleic - protein search, using frame_plus_n2p model

Run on: February 22, 2005, 21:02:19 ; Search time 31 Seconds

(without alignments)

2880.009 Million cell updates/sec

Title: US-09-920-953-2

Perfect score: 1067

Sequence: 1 GCGCTGCTGCGAGCGGC.....AGCATTTCGACCAAGCC 598

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 1027090

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-LOOPEXT=0 -UNITS=bites -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09920953@cgn_1_1_33@runat_17022005_103111_6324 -NCPU=6 -ICPU=3
-NO MMAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSFBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	232	21.7	126	4	US-09-902-540-13031
C 2	136	12.1	345	4	US-09-252-991A-32377
C 3	134.5	12.0	170	4	US-09-252-991A-19980
C 4	134	11.9	663	4	US-09-252-991A-30843
C 5	130.5	11.6	308	4	US-09-252-991A-27249
C 6	129	12.1	1476	4	US-09-252-991A-29427
C 7	126	11.2	235	4	US-09-252-991A-24046
C 8	125.5	11.8	394	4	US-09-252-991A-19344
C 9	124	11.6	312	4	US-09-252-991A-19787
C 10	122	11.4	726	4	US-09-252-991A-20675
C 11	121.5	11.4	204	4	US-09-252-991A-17837
C 12	121.5	11.4	351	4	US-09-252-991A-18476

13	121	11.3	248	4	US-09-252-991A-20161	Sequence 20161, A
14	121	11.3	686	4	US-09-252-991A-20509	Sequence 20509, A
C 15	120	10.7	219	4	US-09-252-991A-23215	Sequence 23215, A
C 16	119.5	10.7	209	4	US-09-252-991A-24725	Sequence 24725, A
17	119.5	11.2	266	4	US-09-252-991A-32478	Sequence 32478, A
18	119.5	11.2	720	4	US-09-252-991A-32006	Sequence 32006, A
19	119	11.2	222	4	US-09-252-991A-26487	Sequence 26487, A
C 20	118.5	10.6	247	4	US-09-252-991A-26899	Sequence 26899, A
21	118	11.1	536	4	US-09-252-991A-20771	Sequence 20771, A
22	118	11.1	565	4	US-09-252-991A-20122	Sequence 20122, A
23	117.5	11.0	273	4	US-09-252-991A-30433	Sequence 30433, A
24	117	11.0	153	4	US-09-252-991A-20543	Sequence 20543, A
25	117	11.0	204	4	US-09-252-991A-21783	Sequence 21783, A
C 26	116.5	10.4	191	4	US-09-252-991A-25365	Sequence 25365, A
27	116.5	10.9	326	4	US-09-252-991A-18751	Sequence 18751, A
C 28	116.5	10.4	335	4	US-09-252-991A-23674	Sequence 23674, A
C 29	116.5	10.9	977	4	US-09-252-991A-16655	Sequence 16655, A
C 30	116	10.3	160	4	US-09-252-991A-30765	Sequence 30765, A
31	116	10.9	297	4	US-09-252-991A-28217	Sequence 28217, A
32	116	10.9	369	4	US-09-252-991A-20790	Sequence 20790, A
33	115.5	10.8	172	4	US-09-252-991A-20172	Sequence 20172, A
34	115	10.8	266	4	US-09-252-991A-19128	Sequence 19128, A
35	115	10.8	681	4	US-09-252-991A-21837	Sequence 21837, A
36	114.5	10.7	143	4	US-09-252-991A-25813	Sequence 25813, A
37	114.5	10.7	168	4	US-09-252-991A-23614	Sequence 23614, A
C 38	114.5	10.2	173	4	US-09-252-991A-33359	Sequence 33359, A
C 39	114.5	10.2	200	4	US-09-252-991A-24828	Sequence 24828, A
C 40	114.5	10.7	474	4	US-09-252-991A-16788	Sequence 16788, A
41	114	10.7	320	4	US-09-252-991A-24634	Sequence 24634, A
42	114	10.7	480	4	US-09-252-991A-31470	Sequence 31470, A
C 43	114	10.2	554	4	US-09-252-991A-28232	Sequence 28232, A
44	114	10.7	697	4	US-09-252-991A-24009	Sequence 24009, A
45	114	10.7	1706	4	US-09-252-991A-31760	Sequence 31760, A

ALIGNMENTS

RESULT 1

US-09-902-540-13031
; Sequence 13031, Application US/09902540
; Patent No. 6833447
; GENERAL INFORMATION:
; APPLICANT: Goldman, Barry S.
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Wiegand, Roger C.
; TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
; FILE REFERENCE: 38-10(15849)B
; CURRENT APPLICATION NUMBER: US/09/902,540
; CURRENT FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: 60/217,883
; PRIOR FILING DATE: 2000-07-10
; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13031
; LENGTH: 126
; TYPE: PRT
; ORGANISM: Myxococcus xanthus
US-09-902-540-13031

Alignment Scores:	3.24e-16	Length:	126
Pred. No.:	232.00	Matches:	51
Score:	56.10%	Conservative:	18
Best Local Similarity:	41.46%	Mismatches:	48
Query Match:	21.74%	Indels:	6
DB:	4	Gaps:	2

US-09-920-953-2 (1-598) x US-09-902-540-13031 (1-126)

Qy 37 ACGCCGAAGCGGATCGCGCGCAAGAGCTGTTTGTACCTGGCGCGCAGAGGC 96
Db 4 ThrAlaGlu-----LysSerValTyrGluInLeuGlyGlyGluProAla 18

[illegible]

US-09-920-953-2 (1-598) x US-09-252-991A-19980 (1-170)

Qy	524	CTGGGCGCGCTCGGCNACTGGCGCTCCCGCTCAA-----AATCATGAATAGTCGC	471
		:::	:::
Dd	14	ProGlyArgAsnArgAlaAlaProAlaAlaAlaGlyArgSerAlaArg	33
		:::	:::
Qy	470	TCAGGTGG-----GGTGGGTTAATAAAAAACAGTTGGTGCGCAGTTGTTGGGNAAG	417
		:::	:::
Dd	34	SerGlyTrpProCysGlyTrp-----Arg-TrpSerHisProCysTrp----	47
Qy	416	TCAAAATTCTGCGGGTGGACTCCACCACCTCCGGCGCGTGCTGGATCAATCTCGTTG	357

Db 48 GlnHisArgArgArgProArgProSerArgArg-----SerArgProAlaAla 64
QY 356 AGCCCACTCTTGAGCGCTCTCCAGGTTACTGTTGATCTTCTCAAGTGGCGGTGG 297
Db 64 aArgPro-----SerGlyGlyAl 70
QY 296 TCCAGCGCGTGGCCCTTGACACAGAT-----GGCGGTGGCGTGCATGCTTCGG 246
Db 70 alaIleArgArgProValProAspGlyGlnProGlyArgArgAsnAlaCys----- 88
QY 245 CCCTTGATTGTTGCTGCTCCGCCAACACAGAGCTCATGAACCTTGACCTGCTTCATCTC 186
Db 89 -----SerThrArg----- 91
QY 185 TGCTCTTGATGTCAGGAGCTCGA-----AGAAGGCGACGAC 147
Db 92 -----LeuProGlyArgArgArgPheProTrpArgProThrArgArgSerAl 108
QY 146 TCCGGGTGAG-----CCAGCACCTTATCGTAGA-----AG 117
Db 108 aProGlySerArgThrGluArgAlaProSerProAlaArgArgGlySerArgArgSerAr 128
QY 116 GTGTCAACCGCCAGCTTCATGCTTCTGCGCGCCAGGTCAATCAACAGCTTCTTGGCG 57
Db 128 gArgArgProAlaAla-----ArgArgGlyThrLeuProCysProAlaCysSe 144
QY 56 CGCATCCGCTTCCGC-----CGTCTCTGT-----GGTGTGGTGGCGGTCTGC 10
Db 144 r-AlaSerArgAsnArgSerArgSerCysSerArgSerGlySerAlaGlyArgSerCys 163

RESULT 4

US-09-252-991A-30843
; Sequence 30843, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 30843
; LENGTH: 663
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30843

Alignment Scores:
Pred. No.: 1,62e-05 Length: 663
Score: 134.00 Matches: 53
Percent Similarity: 35.71% Conservative: 17
Best Local Similarity: 27.04% Mismatches: 71
Query Match: 11.94% Indels: 55
DB: 4 Gaps: 13

US-09-920-953-2 (1-598) x US-09-252-991A-30843 (1-663)

QY 512 CGGCACTGGCGTCCCGCTCAAAATCGATGG-----AAT 477
Db 45 ArgArgValProIleArgCysAlaAsnAlaTrpProGlyArgProMetSerThrSer 64
QY 476 GAGCGCTCGCTGGGT-----TGGTTAAAGAAAT 444
Db 65 ArgArgProGlyTrpSerProAlaValProAlaGlyAlaCysCysTrpLysThrArgAsn 84
QY 443 CAGTTGGTGGCAGTTGTTGGGNAAGTCAAAATTCGTGCGGGGTGACCTCCACACTCCG 384
Db 85 ValAlaGlyArgSerAlaThrAspAlaTrpSerSer-----AlaProAlaPro 100

QY 383 GCGCGTCTGATCAGATCAGATCCTGCTTGTGAGCCCATCTCT-----TGCAGCGTCTCT 333
Db 101 AlaAsnCys-----CysCysLeuPheProAlaGlyProSerProAlaSerProAla 117
QY 332 CCAAGGTACTGCTTGTATCTTGTCAAGTGGCGGTGTCAGGCCG-----TGGCCC 282
Db 118 ProAlaAlaCysArg-----ArgTrpProArgAlaAlaCysHisTrpPro 132
QY 281 TTGACAGATGGCGGTGTCGTCGTACATGCTTCCGCC-----TTGTATTGCTGCTGT 228
Db 133 AlaSerAlaTrp-----TrpTrpLeuAlaProAlaArgCysCysTrpProAla 148
QY 227 CGGCAAAACACAGAGCTATGAACTGACCTGCTTCACTTCTGCTTTCATGCTCCAGG 168
Db 149 ProProAla-----ProAlaSerAlaGlyArgAlaCysCysAlaSe 162
QY 167 GACTCGAAGAAGGCGACGAGCTCCGGTTCAGCAGCACCTTATCGTAGAAGGTGTCAACC 108
Db 162 rProAsnArgArgArgGluProTrpProProSerProTrpAlaSerArgAla---G1 181
QY 107 GCGAGCTTCATGCTTCTGCGCGCCCGAGGTCAATCAACAGCTTCTTGGCGCGCATCCC 48
Db 181 yProAlaSerCys-----GlyArgPro-----ProAlaCysSerProValAl 195
QY 47 GCTTCCGCGCTCTGCTGCTGTGCTGGTGGCGGTCTGACAGGACCG 2
Db 195 aThrAlaProThrAlaThrCysSerProProSerAlaArgSerAla 210

RESULT 5

US-09-252-991A-27249
; Sequence 27249, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 27249
; LENGTH: 308
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-27249

Alignment Scores:
Pred. No.: 2,87e-05 Length: 308
Score: 130.50 Matches: 77
Percent Similarity: 36.59% Conservative: 13
Best Local Similarity: 31.30% Mismatches: 81
Query Match: 11.63% Indels: 75
DB: 4 Gaps: 17

US-09-920-953-2 (1-598) x US-09-252-991A-27249 (1-308)

QY 593 GGTGCGAAAAATGGCTGATGGCTCTTCAATGACAGAGGTGGCAACAGATTTCAGGCT 534
Db 21 GlyAlaGlyProGlyArgGlyGlySer---GlyProGlyArgAlaGlyArgArgSerile 39
QY 533 CTGGGGCCCTGGCGCGCTCGCAACTGGCGTCCCGCTCAAAATCGATGGAATGAG 474
Db 40 ProProAlaProArgArgGlyProArgLeuAlaArgProSerArgGlyArgThr 59
QY 473 CGC-----TCAGGCTGGGTGGGT-----AATGAAATACAGTTG 438
Db 60 ArgAlaProGlyArgCysCysSerGlyTrp---TrpSerThrGlySer-ProMetAlaPr 78

QY 437 GGTGGCGAGTTGTTGGNAAGTCAAATTCGT-----CGCGGTGGACTCCACCACTCG 384
 Db oValArgSerAlaCysArgGlyThrSerArgProValArgSerTrpProGlyProProAl 98
 QY 383 GCGGCGTGTGTCATCAGTCTGCTTGCAGC-----CCATCTCTTGC 342
 Db aglyArgAlaGlyGlyTyArgArgGlyProArgArgSerValProProThrVa 118
 QY 341 AGCTGCTCTCCAAAGTACTGCTTGTACT-----TGTCAAAGTGGCGGTGCTCC 294
 Db lalaSerValAlaGlyProSerArgSerGlyAlaGlyProAlaArgAlaAlaGlyPr 138
 QY 293 AGGCGGTGGCCCTTGACCA----- 275
 Db oGlyAlaAlaProCysProGlyProGlyArgGlySerGlyAlaAlaArgArgHisArgAr 158
 QY 274 -----GATGGCGTGTGCTCGTACATGCTTCGCGCCCTTGTATGCTGCTCGG 225
 Db gGlyArgArgProGlyArgArgSerArgTrpCys-----ProCysAlaGly---SerAr 175
 QY 224 CCAACACGAAGCTCATGAAGTTCGCTGCTTCATCTCTGCTCTTGTGATGTCAGGAC 165
 Db gAlaArgArgProSer-----GlyCysThrGlyCy 185
 QY 164 TCGA-----AGAGGGCA-----GCAGCTCCGGTTCAGCCAGCACCTTA 126
 Db sArgProArgLeuProArgArgAlaGlyArgArgAlaAlaGlyGlyArgProPro----- 203
 QY 125 TCGTAGAGGTCTCAACGCCAGCTTCATGCTTCGCGCCGCCAGGTCATCAA----- 71
 Db -----CysCysProProGlyAla-----ProGlyGluArgLysAr 215
 QY 70 -----ACAGTTCTTCCGCGCCGATCCGCTTCGCGGCTCTGCTGCTGCTGCGCGG 15
 Db gSerThrGluSerSerAlaArg---ProAlaPro-ArgProCysGlyGlySerGlyArgg 234
 QY 14 TCTGAGCGAGCGGC 1
 Db lAlaAlaArgHisArg 238

RESULT 6

US-09-252-991A-29427
 ; Sequence 29427, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 29427
 ; LENGTH: 1476
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-29427

Alignment Scores:
 Pred. No.: 7,478-05 Length: 1476
 Score: 129.00 Matches: 74
 Percent Similarity: 38.01% Conservative: 10
 Best Local Similarity: 33.48% Mismatches: 91
 Query Match: 12.09% Indels: 46
 DB: 4 Gaps: 13

US-09-920-953-2 (1-598) x US-09-252-991A-29427 (1-1476)

QY 9 TGCAGACGGCGCCACCACGACACAGAGCGCGGAAGC-----GGGATGCGG 56

Db 492 CysArgArgAlaHisArgGlnHisArgGlnAlaAlaAlaAspAlaLeuGlyGlnArg 511
 QY 57 GCGCAAGAAGCTGTTTGTATGACCTGGCGCGCGCAAGGCATGAAGCTGGCGGTTGACAC 116
 Db ThrGlnLeuSerArg---ArgProGlyGlnLeuArgArgAlaProGlyHisArgAlaHis 530
 QY 117 CTTCTACCATGAAGTGTGCTGCTGACCCCGAGTGTGCTCTCTTCGATCCCTCGACAT 176
 Db LeuProGlnLeuGlyAlaAla---ValGlyGlyAlaGlyLeuArgArg-----GlyHis 547
 QY 177 GCAAGACGAGAAGATGAAGCAGCTCAAGTTCATGCTGCTGTTGTCGAGCAGACCA 236
 Db ArgProGlyArgTrpProValGlyLeuValarg-----ArgArgLeuPro 562
 QY 237 ATA-----CAAGGCGCAAGCATGTACGACGACACGCCCATCTGTCTAAGGGCACGG 290
 Db AlaGlyArgGlyThrArgArgGlnGlyThrArgThrArgArgProGlyProGlyProAla 582
 QY 291 CTTGGA-----CCACCGCA-----CTTTGACAAGATCAACAGTA 326
 Db ProGlyAlaGlyAlaAspArgProProAlaPheLeuLeuSerGlyAlaAlaArg 602
 QY 327 CTTTGAGAGACGCTGCAAGAGATGGCGTCAA-----GCAGGATGTATCCAGCACGC 380
 Db Pro---ArgArgAlaGlyProAspArgGlnProProAlaGlyProAspProGlyArg 621
 QY 381 CGCGGAGTGTGAGTCCACCGC-----GACGAATTTGACTTNNCCCAACNA 428
 Db ArgHisArgGlyAlaVal-ThrArgCysGlyAlaGlyThrGluAlaGlyValProArgPr 641
 QY 429 CTGCGCACCACTGATTTTCAATTAACCAACCCAG----- 465
 Db oProGlnProAlaAspGlyAlaThrAlaAlaAspGlnGlnGlyArgAspProGlySerHi 661
 QY 466 ---CCTGAGCGCTCATTCATTCGATTTTGAGCGGGAGCGCGCATTCGCCAGCGCGCCC 521
 Db sProGlyArgAspAlaArgArg-----AlaThrValArgProArgPr 676
 QY 522 AGGGGGCCAGGAGCCTGCAATTCGTTGCGAGCCCTGTCGATTGAAGAGCCATCAG 580
 Db cSerArgProAlaGly-GlnTyrHisProProAlaArgValAlaGlyLysArgHisArg 695

RESULT 7

US-09-252-991A-24046
 ; Sequence 24046, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; PRIOR FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 24046
 ; LENGTH: 235
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-24046

Alignment Scores:
 Pred. No.: 7,81e-05 Length: 235
 Score: 126.00 Matches: 47
 Percent Similarity: 39.16% Conservative: 18
 Best Local Similarity: 28.31% Mismatches: 58
 Query Match: 11.23% Indels: 43
 DB: 4 Gaps: 10

US-09-920-953-2 (1-598) x US-09-252-991A-24046 (1-235)

```

QY 482 TGAATGAGCGCTCAGC---TGG-----GGTTGGTTAATGAATCAG 441
|||:::|||||
Db 26 TrpAspGlyArgSerGlyArgTrpSerArgTyrCysAlaTrp-----40
|||:::|||||
QY 440 TTGGGTGGCGAGTGTGGGNAAGTCAAAATTCGTGGGGTGGAGCTCCACCACTCCGGCG 381
|||:::|||||
Db 41 --GlyCysProSerValAlaProThrArgTrpSerArgGlyCysSerArgSerProPro 59
|||:::|||||
QY 380 GCGTGTGGATCATCTCTGCTTGGAGCCCATCTTTGAGCGCTCTCTCAAGGTACTGC 321
|||:::|||||
Db 60 CysAlaTrpAlaSerSerAlaIleThrProTrpProArgThrArgSerProSer-----77
|||:::|||||
QY 320 TTGATCTTGCAAGTGGCGGTGGTCCAGCGCTGGCCCTTGACCATGGCGGTGGCG 261
|||:::|||||
Db 78 -----ArgArgTyrThrTrp---ArgSerTrp-----CysArgTrpGlyCysArg 91
|||:::|||||
QY 260 TCGTACATGCTTCGGCCCTTGATTGTCTGCTCCGCCAAACACGAAGCTCATGAACCTTG 201
|||:::|||||
Db 92 -----ThrProProPro-Thr-----96
|||:::|||||
QY 200 ACTGCTTCACTTCTGCTTTCATGTCAGGACTCGAAGAGGCGCAGCAGCTCCGG 141
|||:::|||||
Db 97 -----AlaSerAlaSerIleSerAlaProAlaAlaCysSerLysHisAlaAlaProGl 114
|||:::|||||
QY 140 TCAGCCAGCACCTTATCGTAGAGGTGT-----CAACCGCCAGCTTCATGCCT 93
|||:::|||||
Db 114 yValSerAlaSerAlaSerAlaArgCysAlaCysSerSerProGlySerGlyGl 134
|||:::|||||
QY 92 TCTGCGCGCCAGGTTCATCAACAGCTTCTTGCGCCCGCATCCGCTTCGGCGCTCTCT 33
|||:::|||||
Db 134 yCysArgArgProSerSerAlaCysSerSerThrAla---ThrProArgProThrGlyAr 153
|||:::|||||
QY 32 GTGGTGTCTGGTGGCG 17
|||:::|||||
Db 153 gTrpProArgTrpPro 158
|||:::|||||

```

RESULT 8
US-09-252-991A-19344
; Sequence 19344, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19344
; LENGTH: 394
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-19344

Alignment Scores:
Pred. No.: 0.000107 Length: 394
Score: 125.50 Matches: 68
Percent Similarity: 31.82% Conservative: 16
Best Local Similarity: 25.76% Mismatches: 76
Query Match: 11.76% Indels: 104
DB: 4 Gaps: 11

US-09-920-953-2 (1-598) x US-09-252-991A-19344 (1-394)

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QY 17 CGGCCACGACGACGACGACGAGCG-----CGG 43
|||:::|||||
Db 116 ArgProGlyAlaProGluProArgGlyThrProProValGlyProGlySerLeuSerArg 135
|||:::|||||

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QY 44 AAGCGGATGCGGGCCAAAGAGCTGTTTGTATGACCTGGCGG-----CCGAG 91
|||:::|||||
Db 136 ArgLysProAlaGly-AspLeuAla-----ProProArgGlnLeuAlaAspArgPr 152
|||:::|||||
QY 92 AAGCGATGAAGTGGCGGTGGACACCTTCTACGATGAAGTGGCTGGCTGACCCCGAGGTGC 151
|||:::|||||
Db 152 oAlaHisProProGlyGlySerHisLeuGlnLeuProGlyAlaGlyProProGlyArgVa 172
|||:::|||||
QY 152 T-----GCCCTCTTCCGA-----164
|||:::|||||
Db 172 lArgProAlaValSerLeuProProAlaValPheArgLeuHisGlnProAlaValAr 192
|||:::|||||
QY 165 -----GTCCCTGGACATCCAGAGCAGACAGATGAAGCAAGTCAAGTTCATGAGTTCG 217
|||:::|||||
Db 192 gArgProLeuProGlyHisAlaAlaAla-----AlaGlyArgThrHisProGlnAl 209
|||:::|||||
QY 218 TGT-----TGGCGGAGCAGACCAAT 238
|||:::|||||
Db 209 aValProProAlaLeuSerArgArgProAlaGlyAlaProGlyArgArgGlnProAs 229
|||:::|||||
QY 239 ACA-----GGCCGGAAGCATGTACGAGCAGCACACCCCATCTGTCAGGGCCACGGCTCG 295
|||:::|||||
Db 229 pGlnProAspProProProAlaArgProArgLeuProAlaLeuAlaGlyProArgProGl 249
|||:::|||||
QY 296 ACCACCGCCACTTTGCAAGATCAAGCATCAAGCATGACCTTGGAGAGACGCTGCAAGAGATGGCG 355
|||:::|||||
Db 249 yArgProProThrAlaHisGluPheAlaAspProAlaThrProProAlaArgGlyArgAr 269
|||:::|||||
QY 356 TCAA-----359
|||:::|||||
Db 269 gGlnLeuProAlaThrGlnGlyProProAlaAlaArgProGlyAspLeuProProGlySe 289
|||:::|||||
QY 360 ----GCAGGATGTATCCAGCAGCAGCGCGAGTGGTGAGTC-----398
|||:::|||||
Db 289 rGlyArgAlaValAspProGlyHisArgArgAlaAlaArgLeuPheArgAlaLeuGlyLe 309
|||:::|||||
QY 399 ----CACCGCGCAGAAATTTGACTTTCCTTCCCAACA 427
|||:::|||||
Db 309 uProSerArgValGlnGluValAspArgProHisProArgArgVal-----324
|||:::|||||
QY 428 ACTGCGCACCACTGATTTTCAATACCCACCCAGCCTGAGCGCTCATTCATCGAT 487
|||:::|||||
Db 325 -----ProAlaProGlyGlySerLeuLysLeuSerPr 335
|||:::|||||
QY 488 TTTGAGCGGGAGCGCCAGTTGCGAGCGCGCCAGGGCGCCAGGAGCCTGCAAAATCGT 547
|||:::|||||
Db 335 oThrProGlyAspGluAlaArgCysAlaValAlaProTrpArgThrAlaAlaAl 355
|||:::|||||
QY 548 TTGCCAGCCC 557
|||:::|||||
Db 355 aAlaArgPro 358
|||:::|||||

```

RESULT 9
US-09-252-991A-19787
; Sequence 19787, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; CURRENT FILING DATE: 1999-02-18
; PRIOR FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US/09/252,991A
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 19787
; LENGTH: 312
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa

US-09-252-991A-19787

Alignment Scores:
Pred. No.: 0.000142 Length: 312
Score: 124.00 Matches: 59
Percent Similarity: 37.70% Conservative: 13
Best Local Similarity: 30.89% Mismatches: 73
Query Match: 11.62% Indels: 46
DB: Gaps: 11

US-09-920-953-2 (1-598) x US-09-252-991A-19787 (1-312)

QY 9 TGCAGACGGCGCCACACAGACAGACGGCGGAGCGGATCGCGGCGCAGAGCT 68
DB 39 CysArgArgProGluGlnHisAlaProHisArgGlyAspGlyArgAlaTrpArg 57
QY 69 GTTGTAGACCTGGCGGCGCAGAGGAGCATGAGCTGGCGGTGACACCTTCTACGATA 128
DB 58 -----GlyHisArgProSer----- 63
QY 129 GGTGCTGGCTGACCGGAGCTGCTGCCCTTCTTCGAGTCCCTCGACATGCAAGACAGAA 188
DB 64 GlyLeuProArgProGlyArg-----LeuArgAlaSerAlaHisArgAlaGly 80
QY 189 GATGAACAGCGTCAAGTTCATGAGCTTCGTGTTGGCGGAGC-----AGACCAATA 239
DB 81 HisArgAlaGlyGlnArgHisAlaLeuProAlaTrpArgThrAlaArgIleArgProAla 100
QY 240 CAAGGCGGAGCATGTACGACGACACGCCCA-----TCT 275
DB 101 AlaGlyProValAlaAlaThrArgGlnAlaProArgArgAlaLeuHisAlaProGlyAla 120
QY 276 GGTCAAGGCGCGGCTGGACACCGCCACTTTGCAAGATCAAGCAGTACTCTGGAGA 335
DB 121 GlyArgGlyArg-----AlaProValArgArgAspProAlaThrProGlyThr 137
QY 336 GACGCT-----GCAAGATGGCGCTCAAGCAGGATGTATCCAGCAGC 380
DB 138 GlyThrAlaAlaLeuLeuHisAlaArgPheGlyHisLeuAla-----HisArg 153
QY 381 CGCGGAGTGTGGAGTCCACCGCGACGAAATTTGACTTNCACCAACTGGCGCCAA 440
DB 154 ProGlyThrGlyProAlaAlaGlyAlaArgValLeuArgArgProArgLeuArgProGln 173
QY 441 CTGATTTTC---ATTAAACCAACCCAGCTGAGCGCTCATTCATCGATTTTGGCGGG 497
DB 174 ArgLeuHisArgLeuHisProAla-----GlyArgArgProArgSerAlaAlaGly 190
QY 498 GAGCGCCAGTGGCGGAGC---GCGCCGAGGGG 527
DB 191 ArgArgGlnGlyProAlaArgLeuProArgGly 201

RESULT 10
US-09-252-991A-20675
; Sequence 20675, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 20675
; LENGTH: 726
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-20675

Alignment Scores:

Pred. No.: 0.000318 Length: 726
Score: 122.00 Matches: 74
Percent Similarity: 32.13% Conservative: 6
Best Local Similarity: 29.72% Mismatches: 74
Query Match: 11.43% Indels: 95
DB: Gaps: 13

US-09-920-953-2 (1-598) x US-09-252-991A-20675 (1-726)

QY 2 CGCTGCTGCAGACG-----CGGCACACAGACACACAGACGCGGAGCGGATCGG 55
DB 299 ArgAlaLeuArgThrGluArgHisProProAspProGlyArgHis-GlyProProAlaAr 318
QY 56 GCGCGAAGAGCTGTTGTATGATCGCTGGCGGCGCAGAGG-----CATGAAGC 103
DB 318 g-----ProAlaAlaArgArgAlaAlaAlaValGlyGluAl 331
QY 104 TGGC-----GGTTGACACCTTCTACGATAAGTGCTGGC-----TGACCGGAGC 148
DB 331 aGlyAlaAlaGlyGlnGlyProArgArgThrGlyAlaAlaArgThrGlnSerProGlySe 351
QY 149 TGTGCTCCTTCTTCGAGTCCCTGGACATCAAGACAGAGATGAAGCAGGTCAAGTTCA 208
DB 351 rAlaGlySerAlaAlaLeuArgAlaHisArgArgAlaGluGlySerAla-----AlaGl 369
QY 209 TGAGCTTCGTGTT-----TGG----- 224
DB 369 yGluLeuArgAlaArgProGlyProTrpProAlaAlaGlnGlnProAlaSerAlaAlaPr 389
QY 225 -----CGGAGCAGACCAATACAAGG 244
DB 389 oAlaProGlyGluGlyArgGlyThrAlaArgAlaAlaArgArgGlnAlaAlaArgGlnAr 409
QY 245 GCGCAAGCATGTACGACGACACGCCCATCTGCTCAAGGCGCCAGCGCTGGACCCGCC 304
DB 409 gProThrAlaValArgThrAspArgGluAspGlnGlyArgProArgProProPr 429
QY 305 ACTTTGACAA-----GATCAA-----GCGTACCTTGGAGACGCTCAAG 346
DB 429 oProAlaGlnProGluAspGlnProAlaProAlaAlaAlaProGlyArgAspAlaAr 449
QY 347 AGAT----- 350
DB 449 gAspAspProGlnArgThrHisGlyThrAlaProAlaGluGlyAlaAlaGlnProGlnAr 469
QY 351 -----GGGCGCTCAAGCAGGAGTGTATCCAGACGCGCGCGAGTGTGTGAGT 397
DB 469 gGlnProAspHisGlyArgHisGlnProGlyAspProGlyValLeuProArgGlyGlyAl 489
QY 398 CCACCCGCGAGAAATTGACTTNCACCAACTCGCACCACTGATTTTTCATTAACCC 457
DB 489 aArgProArg-----GlnProArgAlaArgGlyArgHisGlyGlnPr 503
QY 458 AACCCCGAGCTGAGCGCTCATTCATGATTTTGGCGGAGCGGAGTTCGCGAGCGC 517
DB 503 o-----HisGlyArgArgHisLeuProAl 512
QY 518 GCCCAGGGGCGCCAGAGCGCTGCAA 542
DB 512 aGlnArgGlyGluProAlaLeuArg 520

RESULT 11
US-09-252-991A-17837
; Sequence 17837, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A

; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 17837
 ; LENGTH: 204
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-17837

Alignment Scores: Length: 204
 Pred. No.: 0.000223
 Score: 121.50
 Percent Similarity: 34.56%
 Best Local Similarity: 27.65%
 Query Match: 11.39%
 DB: 4
 Gaps: 14

US-09-920-953-2 (1-598) x US-09-252-991A-17837 (1-204)

QY 5 TGCTGACAGCGCGCCAGCAGCAGCAGCAGCGCGGATCGGCGCGCAAGA 64
 DB 7 CysSerSerThrArgProProThrProThrTrp-----ProSerAlaAsn 21
 QY 65 AGCTGTTGATGACCTGGCGGCGCAGAGGATGAAGCTGGCGGTGACACCTTCTAG 124
 DB 22 SerMetAlaThrAlaThrProProPheProAlaAlaSerTrpArgArgThr-----Thr 39
 QY 125 ATAAAGTGCTGG-----CTGACCGCGAGCTGC----- 151
 DB 40 SerArgCysCysAlaProAlaThrAspArgSerCysSerThrAlaThrSerGlyIleArg 59
 QY 152 TGCCCTTCTTCGAGTCCCTGACATGCAAGCAGCAGAGATGAAGCAGGTCAAGTTCATGA 211
 DB 60 CysGlyThrSerArgProTrp---AlaGlySerArgProProArgSerSer----- 76
 QY 212 GCTTCGTGTTGGCGGAGCAGCAATACAAAGGCGCAAGCATGTACGCGCACACGCC 271
 DB 77 -----ArgGluProGluProCys-----ArgAlaPro 85
 QY 272 ATCTGTCAGGCGCCAGCGCTGGACCCAGCCACTTTGACAGATCAAGCAGTACCTTG 331
 DB 86 ProTrpSer-----AlaAlaIatrp-----AlaAlaThrCys 95
 QY 332 GAGACGCTGCAAGAGATGGCGTCAAGCAGGATGTATCCAGCAGCGCGCGGAGTGG 391
 DB 96 ProArgProCysSerAlaThrCysSer-----ProProSerTrp 109
 QY 392 TGGAGTCCACCGCGCAGATTTGACTTNCACAACTGGCCACCACTGATTTTCAT 451
 DB 110 ThrLeuProThrProGlySerAlaAlaProAlaCysAlaSerGlyIle----- 126
 QY 452 TAACCCAAACCCAGCTGAGCGCTCATTCCATCGATTTGAGCGGCGCGCCAGTT--- 508
 DB 127 -----SerProAlaThrSerAla---AlaAlaThrTrpProCysGlyArgProProPro 143
 QY 509 -----GCCAGCGCGCCAGCGGCGCCAGGAGCTGCAAAATCGT 547
 DB 144 ArgSerProArgArgGlyTrpSerGluSerMetArgTrpCysTrpGlnProAla----- 161
 QY 548 TTGCAGCCCTTGTGATTAAGAGCCATCAGCCATTTTCGACCAAGCC 598
 DB 162 ---ProAlaThrSerAlaAlaArgProProArgProGlySerArgAla 177

RESULT 12

US-09-252-991A-18476
 ; Sequence 18476, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS

; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 18476
 ; LENGTH: 351
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-18476

Alignment Scores: Length: 351
 Pred. No.: 0.000274
 Score: 121.50
 Percent Similarity: 33.50%
 Best Local Similarity: 28.57%
 Query Match: 11.39%
 DB: 4
 Gaps: 10

US-09-920-953-2 (1-598) x US-09-252-991A-18476 (1-351)

QY 30 CACAGAGACGCGGGAAGCGGATGCGCGCGCAAGAAGCTGTTGTGACCTGGCGCGCGC 89
 DB 131 HisArgAlaAlaGlyArgGlyProAlaAlaGlyProSerGlyProArgProGlyArgArg 150
 QY 90 AGA-----AGGCATGAAGCTGGCGGTGACACCTCTTACGATAAGGT 131
 DB 151 LysProAlaValArgProAlaArgHisAlaAlaProAla----- 163
 QY 132 GCTGGCTGACCGCGAGCTGTCGCTTCTTCGAGTCCCTGGA-----CATGCA 179
 DB 164 -----ProGlyLysAspProArgArgArgArgArgGlyAspGlnGluProHisArg 180
 QY 180 AGACGAGAAGATGAAGCAGGTCAAGTTCATGAGCTTCGTGTTGGCGGAGCAGACCAATA 239
 DB 181 AlaAlaArgArgAlaGlyGlyAlaHis-----ArgProTrpArg---ArgProLeu 197
 QY 240 CAAGGCGCGAGCATGTACGACGACACGCGCATCTGTTCAAGGCGCCACGCGCTGGACCA 299
 DB 198 ProGlyProAspHisProArgGlyGlyGlnProAlaGlyGlyIleProHisAla----- 215
 QY 300 CCGCCACTTTGACAAGATCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGGTCAA 359
 DB 216 -----AlaIleArgArgGlyArgGln 222
 QY 360 -----GCAGGATGTGATCCAGCA-----CGCGCGCGG 386
 DB 223 AlaLeuArgAlaGlyArgGlnProAlaProAspArgProLeuHisArgArgArgArg 242
 QY 387 AGTGGTGGATCCACCGCGCAGCAATTTGACTTNCACCAACTGCCGCCCACTGATT 446
 DB 243 ProGlyAlaValAlaProAlaArgLeuGlyAsnLeuAlaGlyGlnAlaGln----- 260
 QY 447 TTCATTAAACCAACCCAGCGCTGAGCGCTCATTCATCGATTTTGGCGGAGCGCGCAG 506
 DB 261 -----GlyArgArgAla 264
 QY 507 TTGCGC-----AGCGCGCCAGCGGCGCCAGGAGC 536
 DB 265 GlyProArgArgArgArgAlaAlaArgHisLeuArgProProArgArgProArgArg 284
 QY 537 CTGCAATC 545
 DB 285 LeuArgVal 287

RESULT 13

US-09-252-991A-20161
 ; Sequence 20161, Application US/09252991A
 ; Patent No. 6551795

; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 20161
 ; LENGTH: 248
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-20161

Alignment Scores:
 Pred. No.: 0.000271 Length: 248
 Score: 121.00 Matches: 47
 Percent Similarity: 35.11% Conservative: 19
 Best Local Similarity: 25.00% Mismatches: 62
 Query Match: 11.34% Indels: 60
 DB: 4 Gaps: 11

US-09-920-953-2 (1-598) x US-09-252-991A-20161 (1-248)
 QY 2 CGCTCCCTGACGCGGCCACACCA---CCACAGACGCGCGAAGCGGATCGGCG 58
 Db 56 ArgCysAlaArgSerProProAlaGlyProSerThrThrArgArgProAlaSer 75
 QY 59 GCAAGA---AGCTGTTGATGACCTGGCGGCGCAGAGGCGATGAAGTGGCGTTGACA 115
 Db 76 AlaSerIleArgCys-----SerAlaArgValArgLysTrpTrpSerThr 90
 QY 116 CTTCTACATGAAGG-----130
 Db 91 SerAlaThrIleArgLysAsnSerAlaAlaAsnThrLysAlaAlaArgTrpCysArg 110
 QY 131 -----TGCTGCTACCGCGAGC-----TGCTGC-----154
 Db 111 ArgCysAlaCysTrp---ThrArgAsnArgProAlaArgSerCysArgCysValAla 129
 QY 155 -----CCTTCTTCGAGTCCCTGGACATGC 178
 Db 130 ThrArgSerSerAlaProProThrThrProProAlaProThrSerIleProThrProCys 149
 QY 179 AAGACGAGAAGTAAGCAGGTCAAGTTTCATGAGCTTCGTGTTGGCGGAGCAGACCAAT 238
 Db 150 ThrArg-----AlaThrCysAlaAlaSerAlaAla---159
 QY 239 ACAAGGCGGAGAGCATGTACGACGACGCGCCATCTGTCGAAGGCGCACGCGCTGGACC 298
 Db 160 ThrArgGlyArgSerCysAlaThr---ThrLysArgTrpArgSerAlaGlySerThrAla 178
 QY 299 ACCGCCACTTTCACAAAGATCAAGCATACCTGGAGAGACGCTGCAAGAGATGGCGCTCA 358
 Db 179 ProGlyLysSerAlaAlaThrProAlaThrThrAlaArgCys-----TrpSerThr 196
 QY 359 AGCAGAGTGTATCCACGACGCGCGGAGTGGTGGAGTCCACCGCGACCAATTTGACT 418
 Db 197 ProGlnAlaProGlyAlaThrProSerProGlyTrpProAlaSerAlaArgTrpAlaCys 216
 QY 419 TNCACCAACTGCGCACCAACT 442
 Db 217 SerProSerAlaAlaGlnProSer 224

RESULT 14
 US-09-252-991A-20509
 ; Sequence 20509, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:

; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 20509
 ; LENGTH: 686
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-20509

Alignment Scores:
 Pred. No.: 0.000398 Length: 686
 Score: 121.00 Matches: 51
 Percent Similarity: 35.22% Conservative: 5
 Best Local Similarity: 32.08% Mismatches: 47
 Query Match: 11.34% Indels: 56
 DB: 4 Gaps: 9

US-09-920-953-2 (1-598) x US-09-252-991A-20509 (1-686)
 QY 3 GCTGCTGACAGCGGCGCCACGACACACAGACGCGGAGCGGATCGGCGCGCAA 62
 Db 117 AlaAlaCysArgArgGlyAlaTrpHis-----GlyLeuArgProArg 130
 QY 63 GAAGCTGTTGATGACCTGCGGCGCGCAGAGGATGAAGCTGGCGGTTGACACCTTCTA 122
 Db 131 ProAla-----GlyArgArgArgProAlaAlaGlyGly-----142
 QY 123 CGATAAGGTGCTGGTGTGACCGCGAGCTGCTCCCTTTCGAGTCCCTGGACATCAAGA 182
 Db 143 -----GlnArgTyrAlaAlaGluArgCysAlaGlyLeuAlaArg 155
 QY 183 CGAGAGATGAAGCAGGTCAAGTTTCATGAGCTTCGTGTTG-----224
 Db 156 ProAlaProArgThr-----ValAlaArgArgArgProTrpArgHisProArgCysAla 173
 QY 225 -----CGAGCAGACCAATACAAAGGCGCGAGCATGTACGACGACACGCGCCATCTGCT 278
 Db 174 ValProArgGlyArgProAlaAlaGlyAla-----AlaAlaArgArgArgGlyAlaGly 191
 QY 279 CAAGGCGCACGCTGGACACCGCCACTTTTGACAAGATCAAGCATGACCTGGAGAGAC 338
 Db 192 GlyGlyIleGlnProGlyLeuPro-----CysLeuAlaTrpArgAla 205
 QY 339 GCTGCAAGA-----GATGGCGGTCAA 359
 Db 206 AlaAlaArgGlyLeuAlaArgLeuProProGlyGlnProTrpAlaThrGlyAlaArgGln 225
 QY 360 GCAGATGTGATCCAGACGCGCGGAGTGGTGA-----GTCCACCGC 404
 Db 226 ProGlyAlaGlyAlaGlyProArgArgGlyGlyGlyValArgArgThrHisPro 244

RESULT 15
 US-09-252-991A-23215
 ; Sequence 23215, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfield et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190

Query	Result
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98	1
99	1
100	1

No.	Score	Match Length	DB	ID	Description
1	254.5	23.9	124	15	US-10-282-122A-61519
2	148	13.9	324	15	US-10-435-114-58160
3	142.5	13.4	19723	15	US-10-084-846E-5
4	125	11.7	417	16	US-10-437-963-143835
5	123	11.7	19695	15	US-10-084-846E-3
6	124.5	11.1	19662	15	US-10-084-846E-6
7	120.5	11.3	19608	15	US-10-084-846E-8
8	119.5	11.2	276	16	US-10-437-963-166380
9	117.5	11.0	384	15	US-10-425-114-72136
10	117.5	11.0	384	15	US-10-425-114-72137
11	117.5	10.5	19723	15	US-10-084-846E-4
12	116.5	10.4	19652	15	US-10-084-846E-7
13	115.5	10.3	155	16	US-10-437-963-103601
14	115.5	10.8	224	16	US-10-437-963-141171
15	115.5	10.8	517	15	US-10-425-114-63797
16	115.5	10.8	517	15	US-10-425-114-63798
17	115.5	10.8	517	15	US-10-425-114-63800
18	115.5	10.8	728	15	US-10-425-114-63691
19	114.5	10.7	381	15	US-10-425-114-47573
20	114.5	10.7	401	15	US-10-425-114-40384
21	113.5	10.6	398	15	US-10-425-114-46621
22	112	10.5	247	15	US-10-425-114-48205
23	112	10.5	19725	15	US-10-084-846E-4
24	111	9.9	265	16	US-10-437-963-176482
25	110.5	10.4	294	16	US-10-437-963-106950
26	110.5	10.4	432	15	US-10-425-114-55735
27	109.5	10.3	530	15	US-10-425-114-65510
28	109.5	10.3	19662	15	US-10-084-846E-6
29	109	9.7	110	16	US-10-437-963-168168
30	109	10.2	273	15	US-10-425-114-64278
31	109	9.7	354	15	US-10-425-114-57426
32	109	9.7	19695	15	US-10-084-846E-3
33	108.5	10.2	312	15	US-10-425-114-36798
34	108.5	10.2	383	15	US-10-425-114-61224
35	107.5	9.6	337	15	US-10-425-114-53493
36	107.5	10.1	397	16	US-10-437-963-128400
37	107	10.0	437	16	US-10-437-963-132079
38	107	9.5	19725	15	US-10-084-846E-4
39	106.5	9.5	336	15	US-10-425-114-56601
40	106	9.9	320	15	US-10-425-114-70729
41	106	9.4	490	16	US-10-437-963-104973
42	105.5	9.9	223	15	US-10-425-114-38596
43	105.5	9.4	19608	15	US-10-084-846E-8
44	105	9.8	188	16	US-10-767-701-36881
45	105	9.8	285	15	US-10-425-114-50473

RESULT 1

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US-2004-002912A-61519
; Sequence 61519, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cheryl
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlssen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forsyth, R.
; APPLICANT: Xu, H.
; TITLE OF INVENTION: Identification of Esser
; FILE REFERENCE: ELITRA.034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078

```

TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(5313)B
 CURRENT APPLICATION NUMBER: US/10/425,114
 CURRENT FILING DATE: 2003-04-28
 NUMBER OF SEQ ID NOS: 73128
 SEQ ID NO 58160
 LENGTH: 324
 TYPE: PRT
 ORGANISM: Zea mays
 FEATURE:
 OTHER INFORMATION: Clone ID: UC-ZMFLB73219F07_FLI.pep
 US-10-425-114-58160

Alignment Scores: 2.08e-05 Length: 324
 Pred. No.: 148.00 Matches: 62
 Score: 38.10% Conservative: 18
 Percent Similarity: 29.52% Mismatches: 77
 Best Local Similarity: 13.87% Indels: 53
 Query Match: 15 Gaps: 10
 DB: 10

US-09-920-953-2 (1-598) x US-10-425-114-58160 (1-324)

QY 5 TGCCTGCAGACGCGG-----CCACGACGACCAAGAGAGAGCGGCGGAGAGCGG 49
 DB 84 CysAlaArgThrArgAlaArgThrAlaProSerAlaProCysThrArgArgThr 103
 QY 50 GATCGGGCGCAGAGAGCTGTTGATGACCTGGCGCGCAGAGAGCATGAGCTGGCGG 109
 DB 104 SerSerGlySerArgAlaCys-----110
 QY 110 TTGACACCTTCTACGATAAGGTGCTGG-----CTGACCGGAGCTGCTGC 154
 DB 111 -----ProSerAlaAlaThrCysTrpArgTipAlaAlaThrArgSerArgProThrSer 128
 QY 155 CCTTCTTCGAGTCCCTGGACATGCAAGAGCAGAGAGTGAAGGTCAGTTCATGAGCT 214
 DB 129 ProArgTrpGlyProTrpCysProSerProSer---SerCysSerSerSerAla 147
 QY 215 TCGTGTGTCGGGAGCAGACCAATACAGGCGCGGAGCATGTACGACGACGACCGCCATC 274
 DB 148 CysCysSerAlaThrCysSerArgProArg-ProProArgArgArgArgProProGl 167
 QY 275 TGGT-----CAAGGGCGCAGCTGGACCAAGGCGGAGTTCGACAGATCAGAGTACC 328
 DB 167 nGlyThrProArgProProArgPro--ThrSerArgThrSerSerAlaArgSerThr 186
 QY 329 TTGGAGAGACCTGCAGAGA-----TGGGCGTCAAGCAGGATGTGATCC 373
 DB 187 -----SerAlaCysThrArgProAlaAlaThrCysTrpSerThrCysArgAlaThrTrp 204
 QY 374 AGCAGCGCGCGAGTGGTGGAGTCCACCCGCGACGAAATTTGACTTCCCAACAGCTGC 433
 DB 205 AlaCysAlaThrProThrTrpArgProAlaProArgCysThrAlaSerAlaThr--- 223
 QY 434 CACCAACTGATTTTCATTAAACCCAGCCTGAGCGCTCATTCATCGATTTTTCAG 493
 DB 224 -----ProGlnAlaAlaAlaSerGlyThrSerTrpArg 234
 QY 494 -----CGGGAGCGCCAGTTCGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 541
 DB 235 ThrTrpArgProArgAlaAlaSerAlaAlaAlaAlaAlaAlaAlaAlaAlaAla 541
 QY 542 AATCGTTTGCAGCCCTTGTCTGCA 565
 DB 254 GlyArgAlaSerSerAlaThrAla 261

RESULT 3
 US-10-084-846A-5
 ; Sequence 5, Application US/10084846A
 ; Publication No. US20040006026A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei

PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 61519
 LENGTH: 124
 TYPE: PRT
 ORGANISM: Legionella pneumophila
 US-10-282-122A-61519

Alignment Scores: 7.12e-16 Length: 124
 Pred. No.: 254.50 Matches: 49
 Score: 64.10% Conservative: 26
 Percent Similarity: 41.88% Mismatches: 41
 Best Local Similarity: 23.85% Indels: 1
 Query Match: 15 Gaps: 1
 DB: 1

US-09-920-953-2 (1-598) x US-10-282-122A-61519 (1-124)

QY 61 AAGAGCTGTTGATGACCTGGCGCGCAGAGGATGAGTGGCGGTTGACACCTTC 120
 DB 3 GluSerLeuPheGluArgLeuGlyGlnAsnAlaValAsnThrAlaValAspIlePhe 22
 QY 121 TAGATTAAGTGTGGTGTGACCGGAGCTGCTGCTGCTTCTTCTGAGTCCCTGGACATGCAA 180
 DB 23 TyrArgLysMetLeuMetAspArgValAsnTyrPhePheAspValAspMetGlu 42
 QY 181 GAGCAGAGATGAAGCAGGTCAAGTTCATGAGCTTCGTGTTGGCGGAGCAGACCAATAC 240
 DB 43 GlnGlnIleLeuLysGlnLysGlyPheLeuThrMetValPheGlyGlyProAsnGlnTyr 62
 QY 241 AAGGCGGAGAGTGTACGACGACAGCGCCCTGTCAGGCGCCAGCGCTGGACCCAC 300
 DB 63 ThrGlyLysSerMetArgGluGlyHisGlnHisLeuLeu---AlaArgGlyLeuAsnAsp 81
 QY 301 CGCCACTTGCACAGATCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGGCTCAAG 360
 DB 82 SerHisValAspIleValIleGluHisLeuGlyGluThrLeuLysGluLeuGlyAlaAsn 101
 QY 361 CAGGATGTGATCCAGCAGCGCGCGAGTGGTGGAGTCCACCGCGCAGAA 411
 DB 102 GluGluAspIleGlnLysValAlaAlaIleAlaAsnSerValArgGlyAsp 118

RESULT 2

US-10-425-114-58160
 ; Sequence 58160, Application US/10425114
 ; Publication No. US20040034888A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E.
 ; APPLICANT: Cao, Yongwei

APPLICANT: WEITNAUER, GABRIELE
 APPLICANT: MUHLENWEG, AGNES
 APPLICANT: TREPZER, AXEL
 APPLICANT: BECHTHOLD, ANDREAS
 TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
 FILE REFERENCE: 1974-005
 CURRENT FILING DATE: 2003-02-25
 PRIOR APPLICATION NUMBER: PCT/EP01/09815
 PRIOR FILING DATE: 2001-08-24
 PRIOR APPLICATION NUMBER: DE 101 09 166.4
 PRIOR FILING DATE: 2001-02-25
 NUMBER OF SEQ ID NOS: 120
 SOFTWARE: PatentIn Ver. 3.2
 SEQ ID NO 5
 LENGTH: 19723
 TYPE: PRT
 ORGANISM: Streptomyces viridochromogenes
 FEATURE:
 OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
 OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
 US-10-084-846A-5

Alignment Scores:
 Pred. No.: 0.000206 Length: 19723
 Score: 142.50 Matches: 63
 Percent Similarity: 34.96% Conservative: 16
 Best Local Similarity: 27.88% Mismatches: 68
 Query Match: 13.36% Indels: 79
 DB: 15 Gaps: 12

US-09-920-953-2 (1-598) x US-10-084-846A-5 (1-19723)

QY	5	TGCTGACAGCGCGCCACACAGACAGCGGAGCGGATGCGGCGCAAGA	64
DB	4635	CysAlaAlaArgSerProSerPro-----AlaTrpSerThr	4647
QY	65	AGCTGTTGATGACCTGG-----GCGGCGCAGAAGCATGAACTGGCGGTG	112
DB	4648	SerAlaProAlaThrTrpSerTrpThrSerAlaAlaThrAlaProCysTrpArgPro	4667
QY	113	ACACCTTCTACGATAAGTCTGGCTG-----TTGGCGGAGCAGACC	235
DB	4668	ThrProThrGlyProAlaTrpSerGluTrpThrProProProSerSerProArg	4687
QY	140	-----ACCGG-----AGCTGCTGCTTCTTCAGTCCCTGGACATGCAAGCAGACA	190
DB	4688	ProThrArgArgAlaSerSerProThrSerSerHisThrThrCysSerAlaGlyAla	4707
QY	191	TGAAGCAGGTCAAGTTTCATGCTTCTGTG-----TTGGCGGAGCAGACC	235
DB	4708	AlaProArgSerSerProArgSerArgCysSerThrThrCysArgValProTrpSerSer	4727
QY	236	AATACAAGGCGCGAAGCATGTACGACG-----TTGGCGGAGCAGACC	262
DB	4728	CysGlyArgSerAlaAlaCysArgThrThrAlaSerGlyProSerArgAlaIleCysPro	4747
QY	263	-----CACACGCCC-----ATCTGTCAGGCGCCAGCGCTGGACACCGCCACT	307
DB	4748	ArgCysSerThrProAlaProThrThrTrpSerAlaThrSerThrTrpThrThrGly	4767
QY	308	TTGACAGATCAGCAGTACTCTGGAGACGCTGCAAGAGATGGGGTCAAGCAGGATG	367
DB	4768	CysAlaArgSerGly-----TrpProSerAla-----	4777
QY	368	TGATCCAGCAGCGCGCGAGTGGTGG-----AGTCCACCGCGAGAAATTTGACTTNC	421
DB	4778	-----ProAlaArgTrpTrpMetProSerProProSerThr--AlaGluAla	4793
QY	422	CCAACAACCTGGCACCACCACTGATTTTCATTAAACCCAA-----	459
DB	4793	erArgSerCysTrpProAlaAlaAlaProLeuAlaArgSerThrSerArgArgTrpProA	4813

QY	460	-----CCCCAGCCTGAGCGCTCATTCATCGATTTTGAGCGGGAGCGCAGTTCGCGAGCGC	517
DB	4813	laSerAlaProGluArgArg-----ThrCysProThrArgSerS	4826
QY	518	GCCAGGGGGCCCA	531
DB	4826	erProGlyglyPro	4830

RESULT 4
 US-10-437-963-143835
 Sequence 143835, Application US/10437963
 Publication No. US2004012343A1
 GENERAL INFORMATION:
 APPLICANT: La Rosa, Thomas J.
 APPLICANT: Kovalic, David K.
 APPLICANT: Zhou, Yihua
 APPLICANT: Cao, Yongwei
 APPLICANT: Wu, Wei
 APPLICANT: Boukharov, Andrey A.
 APPLICANT: Barbazuk, Brad
 APPLICANT: Li, Ping
 TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 FILE REFERENCE: 38-21(53221)B
 CURRENT APPLICATION NUMBER: US/10/437,963
 CURRENT FILING DATE: 2003-05-14
 NUMBER OF SEQ ID NOS: 204966
 SEQ ID NO 143835
 LENGTH: 417
 TYPE: PRT
 ORGANISM: Oryza sativa
 FEATURE:
 OTHER INFORMATION: Clone ID: PAT_MRT4530_44705C.1.pap
 US-10-437-963-143835

Alignment Scores:
 Pred. No.: 0.00384 Length: 417
 Score: 125.00 Matches: 63
 Percent Similarity: 36.19% Conservative: 13
 Best Local Similarity: 30.00% Mismatches: 74
 Query Match: 11.72% Indels: 60
 DB: 16 Gaps: 10

US-09-920-953-2 (1-598) x US-10-437-963-143835 (1-417)

QY	23	CCAGCACACAGACGCGGAGCGGATGCGGCGCAAGAGCTGTTTGATGACCTGG	82
DB	22	ProThrProHisArgArgGlu-----IleGluArgTrp	32
QY	83	GCGGCGCAGAAGCATGAAGCTGGCGGTTGACACCTTCTACGATAAGGTGCTGGCTGACC	142
DB	33	Leu-----ProTrpArgSerAlaProPro-----ThrThr	43
QY	143	CGAGCTGCTGC-----CCTTCTCGAGTCCCTGGACATGCAAGCAGACA	187
DB	44	GlySerCysSerThrProThrProProProProThrThrThrSer---	62
QY	188	AGATGAAGCAGGTCAAGTTTCATGAGCTTCGTTGCGGAGCAGACCAATACAAAGGCC	247
DB	63	-----SerArgSerLeuProAlaThrProProProAlaProThrLysArgArg---	79
QY	248	GAAGCATGTACGACGACACGCCCATCTGCTCAAGGCGCCACGCGCTGGACCGCCACT	307
DB	80	-----ArgThrThrArgTrp---GlyAlaThr	87
QY	308	TTGACAGATCAAGCAGTACCTTGGAG-----AGACGCTGCAAG	346
DB	88	LeuThrAlaThrSerThrAlaGluAsnSerArgArgArgThrArgArgAlaArgArg	107
QY	347	AGATGGCGCTCAGCAGGAGTGTCCAGCACCGCGGAGTGGTGGAGTCCA-----	400
DB	108	ArgGlyArgSerArgAlaSerSerThrThrProProProThrThrSerProGlyThr	127

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QY 401 ---CCCGCAGCAATTGACTTNNCCCAACAACTCGGCACCCCACTGATTTTCATTACCC 457
Db 128 SerProSerThrProSerAlaAlaProSerThrSerProThrArgAlaSerProPro 147
QY 458 AACCCACCGCTGAGCGCTCATTCATCGATTGAGCGGGAGCGCCAGTTGCGGAGCGC 517
Db 148 TyrArgSerThrSerProSerProPro--ProAlaAlaSerSerAlaSerAlaAla 167
QY 518 GCCACGGGGGCCCA-----GGAGCCCTGCAAAATCGTTTG 550
Db 167 TgProProAlaProThrThrSerProThrArgProProSerGlyGlyCysAlaSerLeuA 187
QY 551 CCAGCCCTGTGTCANTGAAGAGCCA 576
Db 187 laThrProAlaThrThrSerThrPro 195

RESULT 5
US-10-084-846A-3
; Sequence 3, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFFER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 3
; LENGTH: 19695
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 1.
; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
US-10-084-846A-3

Alignment Scores:
Pred. No.: 0.0104 Length: 19695
Score: 125.00 Matches: 57
Percent Similarity: 35.29% Conservative: 15
Best Local Similarity: 27.94% Mismatches: 68
Query Match: 11.72% Indels: 64
DB: 15 Gaps: 11

US-09-920-953-2 (1-598) x US-10-084-846A-3 (1-19695)
QY 2 CGCTGCTGCAGACG---CGGCCACAGCACACAGCGCGGAGCGGATGCGGCG 58
Db 11324 ArgCysAlaGlyThrSerAlaSerProAlaSerThrArgArgSerArgSerProAla 11343
QY 59 GCAGA-----AGCTGTTGATGACCTGGCGCGCGGAGGAGGATGAGC 103
Db 11344 AlaArgThrTrpArgCysGlyAlaAlaSerThrThrTrpAlaAlaGlyArgArg----- 11361
QY 104 TGGCGGTGACACCTTCTACGATAGG-----TGCTGG----- 136
Db 11362 -----SerAlaAlaGlyAsnCysTrpSerSerSerThrProArgPro 11376
QY 137 -----CTGACCCGAGCTGCTCCCTTCTTCGAGTCCTCGGACATGC 178
Db 11377 ProThrSerGlySerSerThrThrArgAlaValCysGlyAlaGlySerThrTrpProPro 11396
QY 179 AAGAGCAGAGATGAACAGTCAGTTCA-----TGAGCTTCGTGTTG 223
Db 11397 AspSerProCysProArgCysSerSerThrThrSerProProAlaSerThrArg 11416

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QY 224 GCGGACGAGC-----AATACAAGGCCGGAAGCATGT 256
Db 11417 AlaThrAlaThrArgSerGlyArgTrpSerValArgTrpSerSerArgAlaProProCys 11436
QY 257 ACAGCCGACACGCCCATCTGGTCAAGGCCACCGGCTGGACACCGCCACTTTGACAAGA 316
Db 11437 CysSerProArgSerThrTrpArgArg-----ProThrGlySerProThrArg 11452
QY 317 TCAAGCAGTACCTTGGAGAGACGCTCCAAGAGATGGCGCTCAAGCAGGAGTGTGATCCAGC 376
Db 11453 SerArgSerThr-----ArgAlaAlaGlySerSerArgAlaProPro 11466
QY 377 ACGCCCGCGAGTGGTGGAGT-----CCACCCCGGAGC--- 409
Db 11467 ArgProSerProTrpAlaAlaThrGlySerTrpProTrpArgProProArgThrCys 11486
QY 410 -----AATTGACTTNNCCCAACAACTGCGCACCACTGATTTTCATTACCCCAAC 460
Db 11487 ArgProProArgLeuArgSerProAlaSerArgGlyProSerProArgTrpThrProArg 11506
QY 461 CCCAGCCTGAGC 472
Db 11507 ProAlaValSer 11510

RESULT 6
US-10-084-846A-6
; Sequence 6, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUHLENWEG, AGNES
; APPLICANT: TREFFER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: Patent In Ver. 3.2
; SEQ ID NO 6
; LENGTH: 19662
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 1: amino acid sequence encoded by coding strand 2.
; OTHER INFORMATION: Start codon: gga, Start position: nucleotide 1.
US-10-084-846A-6

Alignment Scores:
Pred. No.: 0.0116 Length: 19662
Score: 124.50 Matches: 56
Percent Similarity: 33.02% Conservative: 14
Best Local Similarity: 26.42% Mismatches: 64
Query Match: 11.10% Indels: 78
DB: 15 Gaps: 10

US-09-920-953-2 (1-598) x US-10-084-846A-6 (1-19662)
QY 536 GCTCTGCGGCCCTGGCGCGCTGGCAACTGGCG-----CTCCCGCTCAAAATCGATGG 480
Db 19332 AlaProGlyArgProProArgProArgProCysAlaGlyPheProThr----- 19347
QY 479 AATGAGCGCTCAGCGTGGGTTGGGTTAATGAATCAGTTGGGTGGCGCAGTTGTTGGN 420
Db 19348 -----ProGlyProGlyTrp----- 19352
QY 419 AAGTCAAATTCGTCGCGGTGGACTCCACCACTCCCGGGCGGTGCTGATCATCATCC--- 363

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Db 19353 -----AlaAlaAlaCysSerAlaAlaProCysSerCysSerAlaThrSerThr 19368
 QY 362 -----TGCTTGAGCGCCATCTCTTGACGCGTCTCTCCA 330
 Db 19369 ArgCysCysSerGlyArgArgSerArgCysThrAlaCysCysSerCysProCysAlaSer 19388
 QY 329 AGGTACTGC---TTGATCTTGTCAAAGTGGCGG-----TGGTCCAGG----- 291
 Db 19389 ArgArgCysGlyCysAlaGlyAlaThrTyrArgProArgArgTrpTyrArgSerPro 19408
 QY 290 ---CCGTGGCCCTTGACCATGGCGTGGCGTGTACATGCTTGGCCCTTGTATTGG 234
 Db 19409 SerProTrpGlyTrpCysArgTrpProThrAlaAlaGlyGlySerAlaAspThrTrpGly 19428
 QY 233 TCTGCTCCGCCAACACG----- 216
 Db 19429 SerSerProSerProProArgProGlyGlyCysThrGluGlyArgSerProValSer 19448
 QY 215 -----AAGCTCATCAACTTGACCTGCTTCTCATCTCTGCTCTTGCATGTCCAGG 168
 Db 19449 SerProHisGlyArg-SerGlyCysTrpProAlaGlyProArgProAlaAlaGlyProG 19468
 QY 167 GACTCGAAGAGGCGACGACTCGGCTCAGCCAGCACCTTATCGTAGAAGGTGTCAACC 108
 Db 19468 YAspArgGlnAlaLeuSerSerGlySerPro----- 19479
 QY 107 GCCAGCTTCATGCTTCTGCGCGCCAGGTGCATCAACAGCTTCTTGGCGCCGCATCCC 48
 Db 19480 -----ArgArgArgGlyAlaProSerPheSerAlaAlaArgIleAl 19493
 QY 47 GCTTCCG-----CCGTCTCTGTGGTCTGTGGTGG 20
 Db 19493 aaAlaProThrIleProAlaLeuPheCysSerTrp 19504

RESULT 7

US-10-084-846A-8
 ; Sequence 8, Application US/10084846A
 ; Publication No. US20040006026A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WEITNAUER, GABRIELE
 ; APPLICANT: MUHLENWEG, AGNES
 ; APPLICANT: TREFFER, AXEL
 ; APPLICANT: BECHTHOLD, ANDREAS
 ; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
 ; FILE REFERENCE: 1974-005
 ; CURRENT APPLICATION NUMBER: US/10/084, 846A
 ; CURRENT FILING DATE: 2003-02-25
 ; PRIOR APPLICATION NUMBER: PCT/EP01/09815
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: DE 101 09 166.4
 ; PRIOR FILING DATE: 2001-02-25
 ; NUMBER OF SEQ ID NOS: 120
 ; SOFTWARE: Patentin Ver. 3.2
 ; SEQ ID NO 8
 ; LENGTH: 19608
 ; TYPE: PRT
 ; ORGANISM: Streptomyces viridochromogenes
 ; FEATURE:
 ; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
 ; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.

US-10-084-846A-8

Alignment Scores:
 Pred. No.: 0.0284 Length: 19608
 Score: 120.50 Matches: 49
 Percent Similarity: 35.71% Conservative: 16
 Best Local Similarity: 26.92% Mismatches: 92
 Query Match: 11.29% Indels: 25
 DB: 15 Gaps: 7

US-09-920-953-2 (1-598) x US-10-084-846A-8 (1-19608)

QY 20 CCACCAGCACACAGAGCGCGAAGCGGGATCGGGCGCGAAGAAGCTGTTTGTATGACC 79

Db 5430 ProProAla-----SerSerThrArgCysCys----- 5438
 QY 80 TGGCGCGCGCAGAGCATGAAGCTGGCGTTTGACACCTTCTACGATAAAGGTCTGCGCTG 139
 Db 5439 -----ProProAlaSerThrTrpArg-----SerThrAlaAlaCysTrpPro 5452
 QY 140 ACCCGAGTGTGCGCTTCTTCAGTCCCTGGAGATGCAAGAGCAGAGATGAAGCAGG 199
 Db 5453 ArgArgProCysSerProArgThrArg-----ThrSerArgArgArgProGlyArg 5470
 QY 200 TCAGTTTCATGACTTCGTGTTTG-----GCGGAGCAGACCAATACAAAGGCGCGAAGCATGT 256
 Db 5471 SerThrSerArgSerThrAlaThrProThrSerGlyCysSerProTrpCysProAlaCys 5490
 QY 257 AGCAGCCACACGCGCATCTGGTCAAGGGCCAGCGCTGGACACCGCCCATCTTTGACAAGA 316
 Db 5491 ThrSerAsnArgProAlaArgProProThrSerSerTrpProThrArgProArgSerAla 5510
 QY 317 TCAAGCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGCTCAAGCAGGATGTGATCCAGC 376
 Db 5511 ProArgProSerThrSerArgSerThrAlaArgTrpProSerProAsnTrpSerArgAsp 5530
 QY 377 ACCCGCGGAGTGTGGAGTCCACCGCGACGAATTTGACTTCCCAACA-----ACT 430
 Db 5531 TrpProThrSerThrProSerProAlaArgThrArgThrAlaProSerArgArgThr 5550
 QY 431 GCGCACCAACTGATTTTCAATTAACCCAGCGCTGAGCGCTCATTCATCGATTTT 490
 Db 5551 ProArgProThrProCysArgArgThrThrProSerAlaSerCysSerArg----- 5567
 QY 491 GAGCGGGGAGCGCGAGTTCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGTTG 550
 Db 5568 ArgProArgThrProValTrpArgArgProGlyCysProProHisArgSerAlaArgLeu 5587
 QY 551 CCAGCC 556
 Db 5588 ProAla 5589

RESULT 8

US-10-437-963-166380
 ; Sequence 166380, Application US/10437963
 ; Publication No. US20040123343A1
 ; GENERAL INFORMATION:
 ; APPLICANT: La Rosa, Thomas J.
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Cao, Yongwei
 ; APPLICANT: Wu, Wei
 ; APPLICANT: Boukharov, Andrey A.
 ; APPLICANT: Barbazuk, Brad
 ; APPLICANT: Li, Ping
 ; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
 ; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
 ; FILE REFERENCE: 38-21(53221)B
 ; CURRENT APPLICATION NUMBER: US/10/437,963
 ; CURRENT FILING DATE: 2003-05-14
 ; NUMBER OF SEQ ID NOS: 204966
 ; SEQ ID NO 166380
 ; LENGTH: 276
 ; TYPE: PRT
 ; ORGANISM: Oryza sativa
 ; FEATURE:
 ; NAME/KEY: unsure
 ; LOCATION: (1)..(276)
 ; OTHER INFORMATION: unsure at all Xaa locations
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: PAT_MRT4530_65095C.1.pap
 ; US-10-437-963-166380

Alignment Scores:

Pred. No.: 0.0118 Length: 276
 Score: 119.50 Matches: 52

Percent Similarity: 35.08% Conservative: 15
 Best Local Similarity: 27.23% Mismatches: 69
 Query Match: 11.20% Indels: 55
 DB: 16 Gaps: 8

US-09-920-953-2 (1-598) x US-10-437-963-166380 (1-276)

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QY 29 CACAGACGCGCGGAGCGGATCGGGCGCAAGAGCTGTTGATGACCTGGCGGCG 88
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 3 ProArgArgArgArgArgArgileCysThrValArg----- 14
QY 89 CAGAGGATGAGTGGCGGTTGACCTTCTACGATAAGTGCTGCGCCGAGC 148
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 15 -----ArgProThrAlaThrThr-----ThrThrThrSer 25
QY 149 TGCTGCCCTTTCAGTCCCTGGATCGCATGCAAGACAGATGAGCAGGTCAAGTTCA 208
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 26 AlaSerProSerSerSerProThrPro-----GlySerSerProGly 39
QY 209 TGAGCTTCGTGTTGCGGAGCAGACCAATACAAGGCGGAGCATGTACGACG----- 262
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 40 AlaAlaSerCysAlaThrSerSerAlaAlaSerArgAlaThrArgThrSerThrAlaPro 59
QY 263 ---CACAGCCCATCTGTGCAAGGCGCCACGGCTGGACACCGCCACTTTGACCAAGATCA 319
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 60 ProSerSerProSerHisGlySerArgSerProThrThrGlyThrThrSerSerProSer 79
QY 320 AGCATGACTTGGAGAGAGCTGC-----AAGAGATGGCGCTCAAGCAGGATGTGA 370
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 80 ArgSerGlySerCysArgGlyCysPheArgArgArgArgArgArgArgArgArgArg 97
QY 371 TCCAGCAGCGCGCGGAGTGTGGAGTCCACCGCGGACGAATTTGACTTNCACCAACT 430
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 98 -----ProAlaAlaProSerSerAlaSerProThrGly 108
QY 431 GGCACCCCAACTGATTTTCAATTAACCAACCCAGCTGAGCGCTCATTCATCGATTTT 490
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 109 AlaSerThrThrSer-----ProSerProThr----- 117
QY 491 GAGCGGGAGCGCCAGTGTGCGAGCGCGCCGCGGAGCGCGCGGCGCGGAGCGCGCGG 550
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 118 -----ProAlaAlaArgAlaAlaSerGlyAlaProAlaAlaSpGlySer***Cys 133
QY 551 CCAGCCCTTGTCATTGAAGAGCCATCAGCCA 583
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 134 SerGlyArgAlaProArgGluSerSerAlaPro 144

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RESULT 9

US-10-425-114-72136
 ; Sequence 72136, Application US/10425114
 ; Publication No. US20040034888A1

GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong
 ; APPLICANT: Zhou, Yihua
 ; APPLICANT: Kovalic, David K.
 ; APPLICANT: Screen, Steven E.
 ; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128

; SEQ ID NO 72136

; LENGTH: 384

; TYPE: PRT

; ORGANISM: Zea mays

; FEATURE:

; OTHER INFORMATION: Clone ID: LIB3245-558-A1_FLI pep

US-10-425-114-72136

Alignment Scores:

Pred. No.: 0.0201 Length: 384
 Score: 117.50 Matches: 69
 Percent Similarity: 37.95% Conservative: 16
 Best Local Similarity: 30.80% Mismatches: 74
 Query Match: 11.01% Indels: 65
 DB: 15 Gaps: 13

US-09-920-953-2 (1-598) x US-10-425-114-72136 (1-384)

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QY 15 CGCGCCACACGAC-----CACAGACGCGGAGCGGATCGGGCGCAAGAGCT 68
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 54 ArgGlyHisArgHisSerSerHisArgProLeuAlaSerGlyArgGln----- 69
QY 69 GTTTGATGACCTGGCGCGCAGAGGCGCATGAAGCTGCG----- 107
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 70 -----ArgArgArgArgGlyArgAlaGlyArgArgGlyGlyArgGlyGlu 84
QY 108 ---GGTTGACACCTTCTACGA-----TAAGTGCT 134
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 85 ProGlyLeuGlyLeuLeuArgGlyArgGlyProArgAlaAlaArgAspArgGlyAla 104
QY 135 GGCTGACCGGAGCTGCTGCCCTTCTCGAGTCCCTGGACATGCA-----AGAGCA 185
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 105 ArgAspGlyGlyAlaAlaArgValLeuArgAlaAlaGlyArgAlaGluGlyArgAla 124
QY 186 GAAGATGAAGCAGCTCAAGTTTCATGCTTCGTGTTGGCGGAGCAGACCAATACAAGGG 245
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 125 GluGluArgGlyGlyAlaAlaArgValLeuArgValGlyAlaHisGlnGluArgGly 144
QY 246 -----CCGAGCATGTACGACGACACCGCCCATCTGTGTCAGGGGCA 287
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 145 LeuGluGlyGlyValArgProArgAlaAlaArgAlaAlaAlaGlySerArgGlyArg 164
QY 288 CGG-----CCTGGACCGCCACCTTGACAGATCAA 320
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 165 ArgArgAlaArgValArgGluGlnValAlaProGlySerAlaGlyLeu---GlnArgGly 183
QY 321 GCAGTACCTTGGAGAGCGCTGCAAGAGATGGCGGT-----CAAGCAGGATGT 368
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 184 AlaGlyGlyValArgGluSer-----AspGlyArgAlaGlyValGlnAlaGlyAla 201
QY 369 GATCCAGCACCCCGGAGTGTGGAGTCCACCGCGAGCGAAT---TTGACTTNCCAA 425
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 202 Asp---ArgProGluProGluAlaGluAlaArgProAlaAlaArgLeuLeuGlnGlyProA 221
QY 426 CAATGCGCACCCCAACTGATTTTCAATTAACCAACCCAGCGCTGAGCGCTCATTCATCG 485
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 221 spAspLeuHisProAlaGlu-----ProLeuProSerMetProGlu----- 234
QY 486 ATTTTGAGCGGAGCGCGCAGTTCGCGAGCGCGCGGCGCGGAGCGCTGCAATC 545
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 235 -----ProArgProGlyProArgGlyThrAlaGlnGlyArgArgProAspHisP 253
QY 546 GTTTGCCA 553
  |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 253 roValPro 255

```

RESULT 10

US-10-425-114-72137

; Sequence 72137, Application US/10425114

; Publication No. US20040034888A1

GENERAL INFORMATION:

; APPLICANT: Liu, Jingdong

; APPLICANT: Zhou, Yihua

; APPLICANT: Kovalic, David K.

; APPLICANT: Screen, Steven E.

; APPLICANT: Tabaska, Jack E

; APPLICANT: Cao, Yongwei

; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
 ; FILE REFERENCE: 38-21(53313)B

; CURRENT APPLICATION NUMBER: US/10/425,114

; CURRENT FILING DATE: 2003-04-28

; NUMBER OF SEQ ID NOS: 73128
 ; SEQ ID NO 72137
 ; LENGTH: 384
 ; TYPE: PRT
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; OTHER INFORMATION: Clone ID: LIB3061-057-C6_FLI.pep
 US-10-425-114-72137

Alignment Scores:
 Pred. No.: 0.0201 Length: 384
 Score: 117.50 Matches: 69
 Percent Similarity: 37.95% Conservative: 16
 Best Local Similarity: 30.80% Mismatches: 74
 Query Match: 11.01% Indels: 65
 DB: 15 Gaps: 13

US-09-920-953-2 (1-598) x US-10-425-114-72137 (1-384)

QY	15	CGGGCCACACAGC	-----CACAGACGGCGGAGCGGATGCGGGCGCAAGAAGCT	68
DB	54	ArgGlyHisSerHisArgProLeuAlaSerGlyArgGln	-----	69
QY	69	GTTTGATGACCTCGGCGGCAGAGCATGAAGCTGGC	-----	107
DB	70	-----ArgArgArgGlyArgAlaGlyArgGlyGlu	84	
QY	108	---GGTTGACACCTTCTACCA	-----TAAGCTGCT	134
DB	85	ProGlyLeuGlyLeuLeuArgGlyArgGlyProArgAlaArgAspArgGlyAla	104	
QY	135	GGCTGACCGGAGCTGCTCCCTTCCTGAGTCCCTGACATGCA	-----AGAGCA	185
DB	105	ArgAspGlyAlaAlaArgValLeuArgAlaAlaGlyArgAlaGlyArgGlyAla	124	
QY	186	GAAGATGAACAGCTCAAGTTTCATGAGCTTCGTGTTGGCGGAGCAGCAACATACAGGG	245	
DB	125	GluGluArgGlyGlyAlaAlaArgValLeuArgValGlyAlaHisGlnGluArgGlyGly	144	
QY	246	-----CCGAGCATGTAGCAGCGCACGCCCATCTGTCAGGGCCA	287	
DB	145	LeuGluGlyGlyValArgProArgAlaAlaArgAlaAlaAlaAlaGlySerArgGlyArg	164	
QY	288	CGG-----CCTGGACCCAGCCGACCTTTGACAGATCAA	320	
DB	165	ArgArgAlaArgValArgGluGlnValAlaProGlySerAlaGlyLeu	183	
QY	321	GCAGTACCTTGGAGAGACGCTGCAAGAGATGGCGT	-----CAAGCAGGATGT	368
DB	184	AlaGlyGlyValArgGlySer-----AspGlyArgAlaGlyValGlnAlaAlaGlyAla	201	
QY	369	GATCCAGCAGCGCCGCGAGTGTGGAGTCCACCGCGCAGCAAT	-----TTGACTTNCCCAA	425
DB	202	Asp--ArgProGluProGluAlaGluAlaArgProAlaAlaArgLeuGlnGlyProA	221	
QY	426	CAACTGCGCACCACTGATTTTTCATTAACCAACCCAGCCTGAGCGCTCATTTCCATCG	485	
DB	221	spAspLeuHisProAlaGlu-----ProLeuProSerMetProGlu	234	
QY	486	ATTTTGGAGCGGAGCGCGCTGCTCCGAGCGCGCCAGGGGGCGCCAGGAGCCTGCAAAATC	545	
DB	235	-----ProArgProGlyProArgArgGlyThrAlaGlnGlyArgArgArgProAspHisP	253	
QY	546	GTTTGGCCA	553	
DB	253	roValPro	255	

RESULT 11

US-10-084-846A-5
 ; Sequence 5, Application US/10084846A
 ; Publication No. US20040006026A1
 ; GENERAL INFORMATION:
 ; APPLICANT: WEITNAUER, GABRIELE

; APPLICANT: MUHLENWEG, AGNES
 ; APPLICANT: TREPZER, AXEL
 ; APPLICANT: BECHTHOLD, ANDREAS
 ; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
 ; FILE REFERENCE: 1974-005
 ; CURRENT APPLICATION NUMBER: US/10/084,846A
 ; CURRENT FILING DATE: 2003-02-25
 ; PRIOR APPLICATION NUMBER: PCT/EP01/09815
 ; PRIOR FILING DATE: 2001-08-24
 ; PRIOR APPLICATION NUMBER: DE 101 09 166.4
 ; PRIOR FILING DATE: 2001-02-25
 ; NUMBER OF SEQ ID NOS: 120
 ; SOFTWARE: Patent In Ver. 3.2
 ; SEQ ID NO 5
 ; LENGTH: 19723
 ; TYPE: PRT
 ; ORGANISM: Streptomyces viridochromogenes
 ; FEATURE:
 ; OTHER INFORMATION: Protein 3: amino acid sequence encoded by coding strand 1.
 ; OTHER INFORMATION: Start codon: atc, Start position: nucleotide 3.
 US-10-084-846A-5

Alignment Scores:
 Pred. No.: 0.0558 Length: 19723
 Score: 117.50 Matches: 64
 Percent Similarity: 32.91% Conservative: 13
 Best Local Similarity: 27.35% Mismatches: 86
 Query Match: 10.47% Indels: 71
 DB: 15 Gaps: 15

US-09-920-953-2 (1-598) x US-10-084-846A-5 (1-19723)

QY	556	GGCTGGCAAAACGATTTCAGAGCTCTCTGGCGCCCTCGGCGCGCTCGGC	-----	509
DB	16445	GlyAlaGlnArgArgCysHisArgThrGlyProIleGlySerGlyAlaGlyProGly	16464	
QY	508	-----AACTGGCGCTCCCGCTCAAAATCGATGGAATG	476	
DB	16465	ThrAlaAlaArgGlnArgLeuValArgSerArgTrpProMetSerAlaSerAlaPhe	16484	
QY	475	AGCGCTCAGCGTGGGTTTAAATAATCAGTTGGTGGCGAGTTCT	-----	425
DB	16485	SerTrpLeuValGlyArgGly-----SerTrpAlaValSerCysAlaArgThr	16500	
QY	424	-----TCG-----GNAAGTCAAAATTCGT	407	
DB	16501	ProArgProGluProArgTrpArgSerProGlyGlyTrpArgThrSerProCysArg	16520	
QY	406	CGCGGG-----TGAGTCCACCACTCCGCGCGGCTCGATCACATCTGCTTGA	356	
DB	16521	AlaGlySerSerSerTrpThrSerPro--ProArgArgProGlyAsnTrpProThrSer	16539	
QY	355	CGCCCATCTTCACAGCTCTCTCCAGGTACGTGTGATCTTGTCAAAGTGGCGGTGT	296	
DB	16540	ThrProSer-----AlaArgThrArgTrpSerThrProSerAlaAlaThrGlyGlySer	16557	
QY	295	CCAGGCGGTGGCGCTTGACCCAGATGGCGGTGGCGGT-----CGTACATGCTTCGGCCCTTGT	239	
DB	16558	ProAsnGlyThrTrpArgProThrAlaArgCysArgProAlaAlaCysTrpThrArgCys	16577	
QY	238	ATTGGTGTGCTCGCCAAACACCAAGCTCATGAATTCAGCTGCTTCTTCTGCTCTT	179	
DB	16578	GlyGly-----ProArgAlaVal-----ProThrSerSerThrSerAla	16590	
QY	178	GCATGT-----CCAGGACTCGAAGAGG-----	155	
DB	16591	GlnCysTrpSerThrAlaArgProArgProValAsnArgProGlyProArgArgPro	16610	
QY	154	GCAGCAGCTCGGGTCCAGCCAGCACCTTATCTAGTAAGGTGTCAACGCCAGCTTCATGC	95	
DB	16611	GlyArgArgProProThrAlaArgProAsnSerArgAlaArgPro-----Cys	16627	
QY	94	CTTCTG-----CGCCGCCAGGTTCATCAACAGCTTCTTGC-----	59	

Db 16628 TrpArgProProArgAlaSerTrpArgAlaCysCysGlySerProThrTrpPro 16647
QY 58 GCCCGCATCCCGCTCCCGCTCTCTGTGGTGTGGTGGCGG 17
Db 16648 GlyArgAlaProArgSerAlaCysSerAlaGlyTrpPro 16661

RESULT 12

US-10-084-846A-7
; Sequence 7, Application US/10084846A
; Publication No. US20040006026A1
; GENERAL INFORMATION:
; APPLICANT: WEITNAUER, GABRIELE
; APPLICANT: MUELENWEG, AGNES
; APPLICANT: TREFFZER, AXEL
; APPLICANT: BECHTHOLD, ANDREAS
; TITLE OF INVENTION: AVILAMYCIN DERIVATIVES
; FILE REFERENCE: 1974-005
; CURRENT APPLICATION NUMBER: US/10/084,846A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: PCT/EP01/09815
; PRIOR FILING DATE: 2001-08-24
; PRIOR APPLICATION NUMBER: DE 101 09 166.4
; PRIOR FILING DATE: 2001-02-25
; NUMBER OF SEQ ID NOS: 120
; SOFTWARE: PatentIn Ver. 3.2
; SEQ ID NO 7
; LENGTH: 19652
; TYPE: PRT
; ORGANISM: Streptomyces viridochromogenes
; FEATURE:
; OTHER INFORMATION: Protein 2: amino acid sequence encoded by coding strand 2.
; OTHER INFORMATION: Start codon: gat, Start position: nucleotide 2.
US-10-084-846A-7

Alignment Scores:
Pred. No.: Length: 0.0697 19652
Score: 116.50 Matches: 73
Percent Similarity: 32.9% Conservative: 14
Best Local Similarity: 27.6% Mismatches: 93
Query Match: 10.3% Indels: 84
DB: 15 Gaps: 13

US-09-920-953-2 (1-598) x US-10-084-846A-7 (1-19652)

QY 598 GCGTGTGCGAATGCGTGTGCTTCAATGAGC-----AAG 557
Db 6432 GlyTrpProThrArgTrpThrArgProGlyCysProSerProSerProArgValArg 6451
QY 556 GCGTGCACAAAGATTGCGAGGCTCTGGGCCCCCTCGGCGCTCGGCAACTGGCGCTCC 497
Db 6452 ProTrpCysThrProCys-----AlaLeuArgIleThrArgAla 6464
QY 496 CCGCTCAAAATCGATGAATGAGCGCTCAGGTGGGGTTGGTTAATGAAATCAGTTGG 437
Db 6465 Profile-----SerProThrArgArgAlaGlyProMet----- 6475
QY 436 GTGGCGAGTGTGGNAGTCAAAATTCGT----- 407
Db 6476 -----CysTrpSerSerTrpGlyArgProLysArgSerProThrProSerArgAla 6492
QY 406 CCGGGGTGGACT-----CCACCACCTCCGGCGGCTCGTGATCA 368
Db 6493 ProGlyTrpThrArgThrAspValProArgProGlyArgSerThrArgSerGlyPro 6512

QY 367 CATCTGTGTGAGCGCCATCTCTTCAGCGTCTCTCCAGGACTGCTTGATCTTGT--- 311
Db 6513 ArgProLeuThrSerArgSerLeuArgProAlaAlaCysGlyThrAlaProHisThrVal 6532
QY 310 ----CAAAGTGGCGGTGTCAGCGCGTGGCCCTTGACCCAGATGGGGTGTGGTGTGATCA 254
Db 6533 ArgArgSerSerHisGlyProThrThrGlyProProHisAlaGlyProArgMetPro 6552

QY 253 TGCTTCGGCCCTTGATTGCTCTGCTCCGCCAAACACGAAGCTCATGAACCTGACCT--- 197
Db 6553 AlaAlaLeuProGlySerGlyValLeuArgAlaArgSerArgCysArgIleProArg 6572
QY 196 -----GCTTCATCTTCTGCTCTTGCATGTCCAGGACTCCAGAGA--- 158
Db 6573 LeuArgArgProArgAlaArgSerArgProGlySerArgCysProCysProArgArgGlu 6592
QY 157 ---AGGCGACAGCTCCGGGTGAGCCAGCA-----CCTTATCTGTAGAGGTGTCAACCG 107
Db 6593 CysArgSerArgArgProArgProProSerHisProAlaArgThrArgCysArgPro 6612
QY 106 CCAGCT-----TCATGC 95
Db 6613 ThrAlaArgProProGlyThrTrpProAlaProArgValArgArgAlaGlyArgAla 6632
QY 94 CTTCTGCGCGCCCGCAGGTCTCAAAACAGCT----- 65
Db 6633 AlaAlaArgArgProProHisArgSerAlaArgSerArgSerArgThrGlyGluSerArg 6652
QY 64 ---TCTTGGCGCCGATCCCGCTTCCGCGCTCTCTGT---GGTCTGTGTGGCGCGCTCTG 11
Db 6653 ArgSer-ThrProAlaProArgArgAlaArgProAlaProGlyAlaGlyArgArgAl 6672
QY 10 CAGCGACGCGC 1
Db 6672 aArgThrArg 6675

RESULT 13

US-10-437-963-103601
; Sequence 103601, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kowalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 103601
; LENGTH: 155
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_101013C.1.pep
US-10-437-963-103601

Alignment Scores:
Pred. No.: Length: 0.0249 155
Score: 115.50 Matches: 48
Percent Similarity: 36.91% Conservative: 7
Best Local Similarity: 32.21% Mismatches: 49
Query Match: 10.29% Indels: 45
DB: 16 Gaps: 9

US-09-920-953-2 (1-598) x US-10-437-963-103601 (1-155)

QY 385 CGCGGGGTGTGGATCATCTCTGTGAGCGCCATCTTGTGAGCGCTCTCTCAAGGT 326
Db 19 ArgArgAlaProThrHisGluPro-----ProSerSerProArgAlaGlyArgSer 36
QY 325 ACTGCTTGATCTTCTCAAGTGGCGGT-----GGTCCAGCGCGTGC 284
Db 37 ArgSerArgSerCysThrSerAlaProArgArgCysHisArgIleAlaProGlyArgGly 56

283	Qy	-----CCTTGACCAGATGGCGTGTGGTTCGTACATGC	251
57	Db	ArgCysArgArgGlyArgHisArgArgGlyAlaProAlaAlaArgLysArgArgCys	76
250	Qy	TTGGGCCCTTGTATTGGTCTGCTCGCCCAACACGAAGCTCATGAACCTTGACCTGCTTCA	191
77	Db	SerGly-----SerAlaAlaArgArgArgSer-----Gly	88
190	Qy	TCCTCTGCTCTTGCATGTCCA-----GGGACTCGAAGAAGSGCAGCAGCTCGG	143
89	Db	AlaAlaArgProProCysProArgProGlySerGlyArgArgArgArgGlyThrAlaPro	108
142	Qy	GGTGAGCCAGCACCTTATCTAGTAGAAGGTGTCAACCGCCAGCTTCATGCCCTCTGTGGCGCCG	83
109	Db	GlySerProArgGlyArgArgArgArgThrHisPro-----ArgArg	122
82	Qy	CCAGGTCAATCAACAGCTTCTTGTCGCCCGC-----ATCCGCGTT	44
123	Db	GlulGly-----GlyProCysThrArgArgSerArgArgGlySerProProArg	139
43	Qy	CCGCGCTCTGTGTGTGTGGTGGCGG	17
140	Db	ProProSerCysThrCvsLeuValPro	148

RESULT 14

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US-10-437-963-141171
; Sequence 141171, Application US/10437963
; Publication No. US20040123343A1
; GENERAL INFORMATION:
; APPLICANT: La Rosa, Thomas J.
; APPLICANT: Kovalic, David K.
; APPLICANT: Zhou, Yihua
; APPLICANT: Cao, Yongwei
; APPLICANT: Wu, Wei
; APPLICANT: Boukharov, Andrey A.
; APPLICANT: Barbazuk, Brad
; APPLICANT: Li, Ping
; TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53221)B
; CURRENT APPLICATION NUMBER: US/10/437,963
; CURRENT FILING DATE: 2003-05-14
; NUMBER OF SEQ ID NOS: 204966
; SEQ ID NO 141171
; LENGTH: 224
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURE:
; OTHER INFORMATION: Clone ID: PAT_MRT4530_42300C.1.pep
US-10-437-963-141171

```

Alignment Scores:		
Pred. No.:	0.0274	224
Score:	115.50	62
Percent Similarity:	32.74%	Conservative: 12
Best Local Similarity:	27.43%	Mismatches: 70
Query Match:	10.82%	Indels: 8
DB:	16	Gaps: 9

11S-09-920-953-2 (1-598) x 11S-10-437-963-141171 (1-224)

Qy	2	CGTGCCTGCAGACGCGCCACCA	CAGACACCA	CAGACGCGGAAGCGGATGCGGCGCA	61
Db	12	ArgAlaLeuGlnArg-HisGlyHis	ArgHisGlyArgArgGlyAlaArg	-----	29
Qy	62	AGAAGCTCTTTGATGACTCGGCGCGC	GAGAGGATGAAGCTGGCGGTGACACCTTCT	121	
Db	30	-----GlyArgTrpArgArgGlyGlyGlyGlnAlaAsnAr		43	
Qy	122	ACGATAAGGTGCTGGCTGACCGGAGCTGTCGCCCTTCTTGAGTGCCTTGGACATGCACAG		181	
Db	43	aArgProProArgHisProSerCvsArgGlnArgArgArgArgProArgArgArgArg		63	

182	A-----	-GCAGACGATGAAGCAGGTCAAGTTTCATGAGCTTCTGCTTGCGGC	222
Qy			
Dd			
63	gproalaLeuAargProalaaGlyalaHisalaGlyArgValArgProleuaLaLeualaAr	83	
Qy			
Dd			
227	GAGCAGACCAATACAAGGGCCGAAAGCATGTACACGCACACGCCCA-----	272	
Qy			
Dd			
83	glEuLeuthrLeuProLeuProAargProAargArgGlnaProProAargGlyArgAl	103	
Qy			
Dd			
273	-----	TCTGGTCAAGGCCACGCCTGGACCCACCGCC	304
Qy			
Dd			
103	aMetLeuLeuAargHisArgArgArgArgTrpaArgArgArgThrpProPropR	123	
Qy			
Dd			
305	ACTTTGCACAAGCATCAAGCAGTACCCTTGGAGA-----	335	
Qy			
Dd			
123	O-----	ArgaArgAlaIleProTPaArgValArgThrpProValHisAlaArgMe	141
Qy			
Dd			
336	-----	GACGCTGCA-----AGAGATGGCGGTCAAGC	361
Qy			
Dd			
141	tAlaAlaGlyAlaAlaValProalaaThrGlyAspArgArgArgArgGlyArgArgAl	161	
Qy			
Dd			
362	AGGATGTGATCCAGCACGCCCGGAGTGGTGGA-----	415	
Qy			
Dd			
161	alaaLaLeuProGluAlaHisArgSerGlyGlyArgAlaValvalProArg-----	178	
Qy			
Dd			
416	ACTTNCCCCAACACTGGCGACCCCACTGATTTTCATTAAACCCACCCCAGCTTGAGCGCT	475	
Qy			
Dd			
178	-----	-----	178
Qy			
Dd			
476	CATTCATCGATTTTGACGGGGAGCGCCAG-----	517	
Qy			
Dd			
179	-LeuProAargValGlnGlnGlyArgHisAlaGlyHisAlaGlyvalLeuProPropR	198	
Qy			
Dd			
518	GCCCCAGGGGCCAGG	533	
Qy			
Dd			
198	oARaArgAlaProArg	203	
Qy			
Dd			

RESULT 15

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US-10-425-114-63797
; Sequence 63797, Application US/10425114
; Publication No. US20040034889A1
; GENERAL INFORMATION:
; APPLICANT: Liu, Jingdong
; APPLICANT: Zhou, Yihua
; APPLICANT: Kovalic, David K.
; APPLICANT: Screen, Steven E
; APPLICANT: Tabaska, Jack E
; APPLICANT: Cao, Yongwei
; TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
; TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
; FILE REFERENCE: 38-21(53313)B
; CURRENT APPLICATION NUMBER: US/10/425,114
; CURRENT FILING DATE: 2003-04-28
; NUMBER OF SEQ ID NOS: 73128
; SEQ ID NO 63797
; LENGTH: 517
; TYPE: PRT
; ORGANISM: Oryza sativa
; FEATURES:
; OTHER INFORMATION: Clone ID: UC-OSFLM202018F10_FLI.pep
; US-10-425-114-63797

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Alignment Scores:	
Pred. No.:	0.0341
Score:	15.50
Percent Similarity:	35.31%
Best Local Similarity:	28.62%
Query Match:	10.82%
DB:	15
Length:	517
Matches:	62
Conservative:	16
Mismatches:	80
Indels:	61
Gaps:	10

US-09-020-953-2 (1-598) x US-10-425-114-63797 (1-517)

QY 24 CAGCACCAACAGAGCGGGGA-----AGCGGATG 53
 ||||| ::::

us-09-920-953-2.rapb

Fri Feb 25 16:26:58 2005

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Db      89 ArgHisGlyArgAspAlaGlyGlyGluProArgHisProAlaAspArgThrAlaGlyArg 108
QY      54 CGGGCGCAAGAGCTGTTGATGACCTGGCGCGCGCAGAGGCATGAAGCTGGCGGTGA 113
Db      109 HisAlaAspArgGlyGlnHisValProGlyArgArgAlaArgGluArgArgGlyGln 128
QY      114 CACCTT-----CTACGATAAGTGTGCTGACCCCGGAGCTGTGCCCTTCTTGA 164
Db      129 HisCysHisAlaHisHisArgGluAspAlaAlaTrpProGlyAlaArgValLeu----- 146
QY      165 GTCCCTGGACATGCA-----AGAGCA 185
Db      147 GlyProGlyHisAlaGlyValProArgArgAspValAlaAlaAlaValAlaArgArgVal 166
QY      186 GAAGATGAAGCAGGTCAGTTCATCAGCTTCGTGTTGGCGGAGCAGCAACCAATACAAGG 245
Db      167 HisLeuArgLeuProAlaValHisGlnArgValProHisArgGlnProAspGln--- 185
QY      246 CGAAGCATGTACGAGC-----ACAGCCCATCTGCT--- 278
Db      186 LeuArgHisValAlaAspProArgValGlyMetAlaProValAlaAlaArgProArgGlyVal 205
QY      279 -----CAGGGCCACGGCTGGACCCACCTTTGACAGATCAAGCAGTA 326
Db      206 ProGlyArgArgHisGlyGlyArgGlyValHisProGlyHisAlaGlnProGly 225
QY      327 CCTTGGAGAGCGCT-----GCAAGAGATGGCGT 356
Db      226 ProAlaArgGluAlaArgProArgProArgArgAlaProAlaGlyAlaArgGlnGlyArg 245
QY      357 CAAGCAGGATGTATCCAGCAGCCCGCGAGTGGTGGAGTCCACCCGGCAGCAATTGA 416
Db      246 Arg-----ArgArgArgValGlnArgHisProArgArgGly 259
QY      417 CTNCCCAACTGCGCACCACTGATTTTCATTACCCCAACCCCGCTGAGCGTC 476
Db      260 AlaArgProGlnGluArgArgGlyArgValProAlaAspProAla-----AlaArg 276
QY      477 ATTCCTCGATTTTGAGCGGAGCGCCAGTTGCCGCGCGCCAGGGGCGCCAGG 533
Db      277 ValProAlaValProGlyHisGlyHisArgValProGlyValProGlnProHisArg 295

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Search completed: February 22, 2005, 21:26:11
Job time : 129 secs